

FT Modified-site 78..84
 FT /label= Tyrosine_kinase_phosphorylation_site
 FT Region 96..125
 FT /label= Myelin_PO_protein
 FT Modified-site 106..109
 FT /note= "Aen is N-glycosylated"
 FT Domain 155..214
 FT /label= Immunoglobulin_domain
 FT Modified-site 201..204
 FT /note= "Aen is N-glycosylated"
 FT Region 229..283
 FT /label= Myelin_PO_protein
 FT Domain 231..256
 FT /label= Transmembrane_domain
 FT Modified-site 262..269
 FT /label= Tyrosine_kinase_phosphorylation_site
 FT Modified-site 298..301
 FT /note= "Aen is N-glycosylated"
 XX
 PN WO200116319-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 23-AUG-2000; 2000WO-US23522.
 XX
 PR 31-AUG-1999; 99US-0151733.
 PR 01-SEP-1999; 99WO-US20111.
 PR 16-DEC-1999; 99WO-US30095.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 05-JUN-2000; 2000US-0209832.
 XX
 PA (GENTH) GENENTECH INC.
 -XX
 PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2001-226690/23.
 N-PSDB; AAD02924.
 XX
 PT New PRO polypeptides for treating immune related and inflammatory
 PT diseases such as rheumatoid arthritis, systemic vasculitis, asthma,
 PT autoimmune hemolytic anemia, and diabetes mellitus
 XX
 PS Claim 10; Fig 10; 11pp; English.
 XX
 CC The present sequence is PRO5723 protein encoded by DNA82361 cDNA
 CC clone. PRO protein, its agonist or antagonist or its antibody which are
 CC capable of enhancing or inhibiting the proliferation of T-lymphocytes
 CC or of increasing the infiltration of inflammatory cells into a tissue
 CC are useful in the diagnosis and treatment of immune-related diseases
 CC in mammals. The PRO protein is useful for treating systemic lupus
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune hemolytic anaemia, autoimmune chromocytopenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinating disease of the central or peripheral nervous system,
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, autoimmune or immune-mediated skin diseases such as bullous
 CC skin disease, erythema multiforme and contact dermatitis, psoriasis,
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
 CC food hypersensitivity and urticaria, immunologic diseases of the lung
 CC such as eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyper-
 CC sensitivity pneumonitis, transplantation associated diseases such as

CC graft rejection or graft-versus-host-disease.
 XX
 SQ Sequence 352 AA;
 Query Match 91.1%; Score 1238; DB 22; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2,4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRELSITTEPEOMIEKAGETAYVPCRFLLGPEPDGPIIDLEWLS 60
 DB 1 MALLLCFVLLCGVADLTRELSITTEPEOMIEKAGETAYVPCRFLLGPEPDGPIIDLEWLS 60
 QY 61 PADNQRVDVYIILYSGDKIYDDYODLKGRVHFTSNLKSAGASINVTNLQSLDICTYOC 120
 DB 61 PADNQRVDVYIILYSGDKIYDDYODLKGRVHFTSNLKSAGASINVTNLQSLDICTYOC 120
 QY 121 KYRKAAGVGNKKIQLTVLLKPSGTCYVNGSEIENGDFLLKCEPREGSLPLIYENOKLSN 180
 DB 121 KYRKAAGVGNKKIHLVLPKPGARCVDGSEISGDFKIKCEPREGSLPLIYENOKLSD 180
 QY 181 SOKLPTLMLAEMTSPVIVKNASTEYSGTYSCVKNRVGSDQCLRLDVVPPSNRAGTIA 240
 DB 181 SOKMPTSLAEMTSSVIVKNASSSEYSGTYSCVKNRVGSDQCLRLNVPFSPNRAGLIA 240
 QY 241 GAVIGVLLALVLIIGLIIFCCR 261
 DB 241 GAVIGVLLALVLIIGLIIFCCR 261
 RESULT 2
 AAB65294 standard; Protein; 352 AA.
 XX
 AC AAB65294;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO5723 protein sequence SEQ ID NO:505.
 XX
 KM Human; secreted and transmembrane protein; PRO; cytosolic;
 KM cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99WO-US15863.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06684.
 PR 20-MAR-2000; 2000WO-US07377.
 (GENTH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;
 DR MPI: 2001-032160/04.
 DR N-PSDB; AAF44263.
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 318; 935pp; English.
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAF65154 to AAF65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SO Sequence 352 AA:
 Query Match 91.1%; Score 1238; DB 22; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYVPCRTTLPEDQGPDIEMWLS 60
 DB 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYVPCRTTLPEDQGPDIEMWLS 60
 QY 61 PADNOKVDPVITILYSGDKTYDDYDOLKGRVHTSNDLSGASIVNTLQLSDIGTYOC 120
 DB 61 PADNOKVDPVITILYSGDKTYDDYDOLKGRVHTSNDLSGASIVNTLQLSDIGTYOC 120
 QY 121 KYKKA PGVGNKKIQLTVLKPSTGRCYVDGSEIEGDFLKEPEKGSPLLYEMQKLSN 180
 DB 121 KYKKA PGVGNKKIQLTVLKPSTGRCYVDGSEIEGDFLKEPEKGSPLLYEMQKLSN 180
 QY 181 SOKLPTLMLAEMTSPVTSVKNASTESYSGTYCTVKNRVSGDOCLRLDVAVPSNRAQTIA 240
 DB 181 SOKLPTLMLAEMTSPVTSVKNASTESYSGTYCTVKNRVSGDOCLRLDVAVPSNRAQTIA 240
 QY 241 GAVIGVLLALVLIIGLIIFCCR 261
 DB 241 GAVIGVLLALVLIIGLIIFCCR 261
 RESULT 3
 ID AAB50930
 ID AAB50930 standard; Protein; 352 AA.
 AC AAB50930;
 DT 21-MAR-2001 (first entry)
 DE Human PRO5723 protein.
 KW Human; PRO; antiinflammatory; dermatological; antiarthritic;

KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
 KW antidiabetic; nootropic; neuroprotective; hepatotropic; virocidic;
 KW anti-allergic; antiasthmatic; immune related disorder;
 KW hepatobiliary disease; autoimmune disease; allergy.
 XX
 OS Homo sapiens.
 XX WO200073452-A2.
 PN
 XX
 PD 07-DEC-2000.
 XX
 XX 02-JUN-2000; 2000WO-US15264.
 PF
 XX 02-JUN-1999; 99WO-US12252.
 PR 20-JUL-1999; 99US-0144732.
 PR 20-JUL-1999; 99US-0144758.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 09-DEC-1999; 99US-0170262.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 XX
 PA (GENTH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL,
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK,
 PI Wood WI;
 XX
 DR MPI: 2001-025253/03.
 DR N-PSDB; AAC91489.
 XX
 PT Thirty three nucleic acids encoding PRO polypeptides which are useful
 PT in the diagnosis and treatment of immune related disorders, e.g.
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 PT thyroiditis and diabetes mellitus -
 XX
 PS Claim 58; Fig 58; 218pp; English.
 XX
 CC The present sequence is one of thirty three novel PRO polypeptides.
 CC The PRO polypeptides, anti-PRO antibodies, agonists and
 CC antagonists are useful for treating and diagnosing immune related
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
 CC (such as infectious, autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,

CC Food hypersensitivity and urticaria), immunological diseases of the
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
 CC and hypersensitivity pneumonitis), transplant-associated diseases
 CC including graft rejection and graft-versus-host diseases.

XX Sequence 352 AA;

Query Match 91.1%; Score 1238; DB 22; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYVPCFRTLGPEDEGPIDEWLIS 60
 DB 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYVPCFRTLGPEDEGPIDEWLIS 60
 QY 61 PADNOKVDVYIILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120
 DB 61 PADNOKVDVYIILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120
 QY 121 KYKAKGVGNKKIQLTVLLKPSGTRCYVDGSEIEIGDFLKLCEPKESLPLLEYWOKLSN 180
 DB 121 KYKAKGVGNKKIQLTVLLKPSGTRCYVDGSEIEIGDFLKLCEPKESLPLLEYWOKLSN 180
 QY 181 SQKLPFLMLAEMTSPIVSKNASTERYSGTYSCTVKKRVSGDQCLRLDVPSPNRAQTIA 240
 DB 181 SQKLPFLMLAEMTSPIVSKNASTERYSGTYSCTVKKRVSGDQCLRLDVPSPNRAQTIA 240
 QY 241 GAVIGVLLALVILGLIIFCCR 261
 DB 241 GAVIGVLLALVILGLIIFCCR 261

RESULT 4

ID ABB95562 standard; Protein; 352 AA.

AC ABB95562;

DT 19-JUL-2002 (first entry)

XX Human angiogenesis related protein PRO5723 SEQ ID NO: 280.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnary;

XX antiteriosclerotic.

OS Homo sapiens.

PN WO200208284-A2.

PD 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.
 XX 20-JUL-2000; 2000US-219556P.
 XX 25-JUL-2000; 2000US-220624P.
 XX 25-JUL-2000; 2000US-220624P.
 XX 28-JUL-2000; 2000WO-US20710.
 XX 02-AUG-2000; 2000US-222695P.
 XX 17-AUG-2000; 2000US-0643657.
 XX 23-AUG-2000; 2000WO-US23522.
 XX 24-AUG-2000; 2000WO-US23338.
 XX 07-SEP-2000; 2000US-230978P.
 XX 15-SEP-2000; 2000US-000000P.
 XX 18-SEP-2000; 2000US-0664610.
 XX 18-SEP-2000; 2000US-0665350.
 XX 24-OCT-2000; 2000US-242922P.
 XX 08-NOV-2000; 2000US-0709238.
 XX 08-NOV-2000; 2000WO-US30952.
 XX 10-NOV-2000; 2000WO-US30873.
 XX 01-DEC-2000; 2000WO-US32678.
 XX 20-DEC-2000; 2000US-0747259.

PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-080689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.

XX (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERE) FERRARA N.
 PA (GERE) GERBER H.
 PA (GERE) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODD) GODDARD P J.
 PA (GURNE) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WFI; 2002-171999/22.
 DR N-PSDB; ABL95700.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 11; Fig 280; 567pp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thromboplastic, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 352 AA;

Query Match 91.1%; Score 1238; DB 23; Length 352;
 Best Local Similarity 89.3%; Pred. No. 2.4e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYVPCFRTLGPEDEGPIDEWLIS 60
 DB 1 MALLLCFVLLCGVADITRSLSTTPPEOMIEKAGETAYVPCFRTLGPEDEGPIDEWLIS 60
 QY 61 PADNOKVDVYIILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120
 DB 61 PADNOKVDVYIILYSGDKTYDDYODLKGKRVHFTSNDLKSASINVTNLQSLDGTGYOC 120


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OY 121 KYKAPGVGNKKIQLTVLKPSTGRVCYDGSSEIIGNDFLKCPEKSGSLPLYEMOKLSN 180
DB 121 KYKAPGVGNKKIHLVVLKPSGARCVDGSEIIGSDPFKICEPKGSLPLYEMOKLSN 180
OY 181 SOKLPTLMLAEMTSPVIVSNASTESGTYSCVKNRVSGDCLRLDVPVPENRAGTIA 240
DB 181 SQMPTSLAEMTSSVIVSNASTESGTYSCVKNRVSGDCLRLDVPVPENRAGTIA 240
OY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 5
AB84956
ID ABB84956 standard; Protein; 352 AA.
XX
AC ABB84956;
XX
DT 16-MAY-2002 (first entry)
DE Human PRO5723 protein sequence SEQ ID NO:280.
XX
XX Human: angiogenesis; cardiac; cytostatic; antiangiogenic; hypotensive;
XX vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
XX WO200200690-A2.
XX
PD 03-JUN-2002.
XX
PF 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001US-0866028.
XX 25-MAY-2001; 2001US-0866034.
XX 30-MAY-2001; 2001US-0870922.
XX 30-MAY-2001; 2001US-0870574.

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PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gertsen ME, Goddard A,
PI Godowski PJ, Gueney AL, Hillan KJ, Matsters SA, Pan J, Paoni NF,
PI Stephan UF, Watanabe CK, Williams PW, Wood WI, Ye W;
XX WPI; 2002-090516/12.
XX DR N-PSDB; ABL88211.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 280; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumor angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
SQ Sequence 352 AA;
XX
XX Query Match 91.1%; Score 1238; DB 23; Length 352;
XX Best Local Similarity 89.3%; Pred. No. 2.4e-108;
XX Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
XX
OY 1 MALLLCFVLLCGVADLTRSLSTTPEOMTEKAGETAYVPCRFLLGPEDQGPDIEMLS 60
DB 1 MALLLCFVLLCGVADFPARSLSTTPEMEKAGETAYVPCRFLLSPEDQGPDIEMLS 60
OY 61 PADNOKVDVIIILYSGDKYIDYDYLKGRVFTSNDLKSQASINVTNLQSDIGTYOC 120
DB 61 PADNOKVDVIIILYSGDKYIDYDYLKGRVFTSNDLKSQASINVTNLQSDIGTYOC 120
OY 121 KYKAPGVGNKKIQLTVLKPSTGRVCYDGSSEIIGNDFLKCPEKSGSLPLYEMOKLSN 180
DB 121 KYKAPGVGNKKIHLVVLKPSGARCVDGSEIIGSDPFKICEPKGSLPLYEMOKLSN 180
OY 181 SOKLPTLMLAEMTSPVIVSNASTESGTYSCVKNRVSGDCLRLDVPVPENRAGTIA 240
DB 181 SQMPTSLAEMTSSVIVSNASTESGTYSCVKNRVSGDCLRLDVPVPENRAGTIA 240
OY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 6
AA69697
ID AAM69697 standard; Protein; 365 AA.
XX
AC AAM69697;
XX
DT 07-DEC-1998 (first entry)
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
XX
XX HCAR, coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
XX Ad5 receptor; human; infection; vaccine; therapy.
XX
XX

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OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 35..130
XX FT Domain /note= "extracellular immunoglobulin domain"
XX FT 155..220
XX FT Domain /note= "extracellular immunoglobulin domain"
XX FT 45..52
XX FT Region /note= "CVB binding region (Claim 6)"
XX FT 47..51
XX FT Region /note= "Ad2/5 and CVB binding region (Claim 6)"
XX FT 53..57
XX FT Region /note= "Ad2/Ad5 binding region (Claim 6)"
XX FT 69..73
XX FT Region /note= "Ad2/Ad5 binding region (Claim 6)"
XX FT 72..77
XX FT Region /note= "Ad2/5 and CVB binding region (Claim 6)"
XX FT 72..77
XX FT Region /note= "CVB-binding region (Claim 6)"
XX FT 77..79
XX FT Region /note= "Ad2/Ad5 binding region (Claim 6)"
XX FT 96..100
XX FT Region /note= "CVB-binding region (Claim 6)"
XX FT 122..127
XX FT Region /note= "Ad2/5 and CVB binding region (Claim 6)"
XX
XX MO9833819-A1.
XX
XX PD 06-AUG-1998.
XX
XX PF 30-JAN-1998; 98WO-US01724.
XX
XX PR 30-JAN-1997; 97US-0036986.
XX
XX PA (UANY ) UNIV NEW YORK STATE.
XX
XX PI Philipson L, Tomko RP.
XX
XX DR WPI; 1998-437397/37.
XX
XX DR N-PSDB; AAV50429.
XX
XX PT DNA encoding human receptor for adenovirus C and coxsackievirus B -
XX PT for preventing and treating viral infection and rendering cells
XX PT susceptible to transformation by adenoviral vectors in gene therapy
XX
XX PS Claim 3; Page 67-68; 88pp; English.
XX
XX CC This is the amino acid sequence of human HCAR, a protein that
XX CC serves as a cellular receptor for adenoviruses of the serotypes 2
XX CC and 5 (subgroup C) and for the group B coxsackieviruses (CVB). The
XX CC sequence was deduced from an isolated cDNA clone for HCAR (see
XX CC AAV50429). The invention also provides host cells transformed with
XX CC DNA molecules encoding HCAR or mouse mCAR (see AAM69698) and methods
XX CC of producing the recombinant proteins or their derivatives. These
XX CC proteins, their extracellular domains, as well as oligopeptides
XX CC (see AAM69699-708) which bind virus, are claimed. Isolated HCAR or
XX CC mCAR proteins or their fragments or variants are used to prevent or
XX CC treat virus infections and for inhibiting the infectivity of Ad2,
XX CC Ad5 or CVB. Methods are also provided for detecting or measuring
XX CC the quantity of HCAR or mCAR in a sample, and for identifying
XX CC analytes capable of binding to HCAR or mCAR.
XX
XX SO Sequence 365 AA;
XX
XX Query Match 91.1%; Score 1238; DB 19; Length 365;
XX Best Local Similarity 89.3%; Pred. No. 2.6e-108;
XX Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
XX
XX QY 1 MALLLCGVLLCGVADLRSLSTTPPEOMIKAKGETYVLCRFTGPDGSPDLDEWLS 60
XX 1 MALLLCGVLLCGVADLRSLSTTPPEOMIKAKGETYVLCRFTGPDGSPDLDEWLS 60
XX DB 1 MALLLCGVLLCGVADLRSLSTTPPEOMIKAKGETYVLCRFTGPDGSPDLDEWLS 60
XX QY 61 PADNOKVDVILLYSGDKIYDDYQDLKGRVHFTSNDLKSQDASINVTNLQLSDIGTYQC 120

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DB 61 PADNOKVDVILLYSGDKIYDDYQDLKGRVHFTSNDLKSQDASINVTNLQLSDIGTYQC 120
QY 121 KYKAPGVGNKKIQLVLLKPSGTRCYVDGSEIGNDFLKCEPKEGSLPLYEMOKLSN 180
DB 121 KYKAPGVGNKKIHLVLLKPSGTRCYVDGSEIGNDFLKCEPKEGSLPLYEMOKLSN 180
QY 181 SQKLPFLWLAEMTSPVSVKNASSTEGYSGCTVKNRVSGDCLRLDVPVPSNAGTIA 240
DB 181 SQKLPFLWLAEMTSPVSVKNASSTEGYSGCTVKNRVSGDCLRLDVPVPSNAGTIA 240
QY 241 GAVIGVLLALVLLGLIFCCR 261
DB 241 GAVIGVLLALVLLGLIFCCR 261

RESULT 7
AAM57212
ID AAM57212 standard; Protein, 365 AA.
XX
XX AC AAM57212;
XX
XX DT 03-AUG-1998 (first entry)
XX
XX DE Human coxsackievirus and adenovirus receptor.
XX
XX KW Human; coxsackievirus; adenovirus; receptor; CAR; cardiac infection;
XX KW myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
XX KW pancreatic infection; acute pancreatitis; gastrointestinal tract;
XX KW diabetes mellitus.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 188
XX FT /note= "encoded by TCG"
XX
XX PN MO9811221-A2.
XX
XX PD 19-MAR-1998.
XX
XX PF 12-SEP-1997; 97WO-US16189.
XX
XX PR 13-SEP-1996; 96US-0026100.
XX
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX
XX PI Bergelson JM, Finberg RW, Horowitz MS;
XX
XX DR WPI; 1998-207384/18.
XX
XX DR N-PSDB; AAV28845.
XX
XX PT DNA encoding coxsackie virus and adenovirus receptor - useful for
XX PT modulation of e.g. cardiac, pancreatic or gastrointestinal infection
XX
XX PS Claim 12; Fig 1B; 104pp; English.
XX
XX CC The present sequence represents human coxsackievirus and adenovirus
XX CC receptor (CAR). The present invention also describes: (1) a method for
XX CC modulating CAR expression comprising contacting the cell with an agent
XX CC which modulates CAR protein activity or CAR nucleic acid expression,
XX CC such that a cell associated activity is altered relative to a cell
XX CC associated activity of the cell in the absence of the agent; and (2) a
XX CC method for detecting the presence of CAR in a biological sample
XX CC comprising contacting a biological sample with an agent capable of
XX CC detecting CAR protein or mRNA such that the presence of CAR is detected.
XX CC Modulation of CAR is useful for treatment of cardiac infection, e.g.
XX CC myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
XX CC central nervous system, e.g. a non-specific febrile illness or
XX CC meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
XX CC or infection of the respiratory or gastrointestinal tract or childhood
XX CC onset diabetes mellitus. Probes derived from CAR nucleic acids are
XX CC useful for hybridisation assays, and antibodies raised against CAR

```

CC protein are useful for blocking CAR expression. Cell-free assays which
CC include combining CAR protein and a candidate/test compound are useful
CC in screening for drugs which interact with CAR protein.

XX Sequence 365 AA;

Query Match 91.1%; Score 1238; DB 19; Length 365;
Best Local Similarity 89.3%; Pred. No. 2.6e-108;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTTPROMTEKAKGATAYLPCRFITGEPDQGLDIEWLIS 60
DB 1 MALLLCFVLLCGVADLTSLSTTPROMTEKAKGATAYLPCRFITGEPDQGLDIEWLIS 60
QY 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQJSDIGTYOC 120
DB 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQJSDIGTYOC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVNGSEIENDFKLCKEPEKGSPLPLYEMOKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVNGSEIENDFKLCKEPEKGSPLPLYEMOKLSN 180
QY 181 SOKLPTLWLAEMTSSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLNVPSPNKAQTIA 240
DB 181 SOKLPTLWLAEMTSSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLNVPSPNKAQTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 8
AAB47270
ID AAB47270 standard; Protein; 365 AA.

XX AAB47270;

DT 06-AUG-2001 (first entry)

DE Human CAR.

KM Coxsackie virus and/or Adenovirus receptor; CAR; transgenic mouse;
KW transgene; tCAR; transduction; integrin; gene transfer; lymphocyte;
KW lymphocyte-specific transcription regulatory sequence; T cell.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Protein 1..262

FT /note= "Claimed tCAR"

XX US6245966-B1.

PD 12-JUN-2001.

PF 19-MAR-1999; 99US-0272496.

PR 14-JUL-1998; 98US-0092782.

PA (UYTE-) UNIV TECHNOLOGY CORP.

PI Degregori J;

DR MPI: 2001-36549/38.

DR N-PSDB; AAC85813.

PT Transgenic mouse comprising a nucleotide sequence encoding a truncated
PT Coxsackie virus and/or Adenovirus receptor (tCAR) polypeptide useful for
PT the analysis of cellular physiology -

PS Claim 3; Column 15-18; 21pp; English.

XX This sequence shows a Coxsackie virus and/or Adenovirus receptor (CAR)

CC polypeptide. The DNA encoding this sequence was used in the method of
CC the invention to produce a transgenic mouse whose genome comprises a
CC transgene comprising a nucleotide sequence encoding a truncated CAR
CC polypeptide (tCAR) operably linked to a lymphocyte-specific
CC transcription regulatory nucleotide sequence. The tCAR is expressed
CC in the lymphocytes of the mouse at levels sufficient for increased
CC susceptibility to adenoviral transduction of the lymphocytes without
CC affecting the expression of endogenous integrins in the lymphocytes.
CC The transgenic mouse is useful for the analysis of pathways, via gene
CC transfer, which control various aspects of cellular physiology either
CC in vitro or in vivo. The tCAR-regulatory sequence construct facilitates
CC either the in vivo delivery of genes into T cells by the inoculation of
CC adenovirus recombinants into lymphoid organs or the ex vivo delivery of
CC genes into transgenic T cells as T cells expressing the truncated form
CC of tCAR are highly efficient target cells for adenoviral transduction.

XX Sequence 365 AA;

Query Match 91.1%; Score 1238; DB 22; Length 365;
Best Local Similarity 89.3%; Pred. No. 2.6e-108;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTTPROMTEKAKGATAYLPCRFITGEPDQGLDIEWLIS 60
DB 1 MALLLCFVLLCGVADLTSLSTTPROMTEKAKGATAYLPCRFITGEPDQGLDIEWLIS 60
QY 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQJSDIGTYOC 120
DB 61 PADNOKVDQVILLYSGDKIYDDYODLKGKRVHFTSNDLKSASPASINVTNLQJSDIGTYOC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVNGSEIENDFKLCKEPEKGSPLPLYEMOKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVNGSEIENDFKLCKEPEKGSPLPLYEMOKLSN 180
QY 181 SOKLPTLWLAEMTSSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLNVPSPNKAQTIA 240
DB 181 SOKLPTLWLAEMTSSVIVKNASTEYSGTYSCTVKNRVGSDOCLRLNVPSPNKAQTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 9
ABB08040
ID ABB08040 standard; Protein; 365 AA.

XX ABB08040;

DT 27-AUG-2002 (first entry)

DE Human coxsackie-adenovirus receptor (CAR).

KM Targeting molecule; adenoviral receptor domain; trimerisation; cancer;
KW coxsackie-adenovirus receptor; CAR; transmembrane protein; cytoskeletal;
KW hepatotropic; virucide; gene therapy; human; receptor.

OS Homo sapiens.

XX WO200229072-A2.

PN 11-APR-2002.

PF 05-OCT-2001; 2001WO-EP11514.

PR 06-OCT-2000; 2000US-327562P.

PR 06-OCT-2000; 2000US-0684552.

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Kim JG, Smith T, Stevenson SC, Kaleko M;

DR WPI; 2002-471317/50.
 DR N-PSDB; ABL60622.
 XX
 PT A targeting molecule for use in forming complexes to treat cancer, such
 PT as adenocarcinoma of the prostate, comprises a soluble adenoviral
 PT receptor domain, a trimerization domain and a targeting ligand domain -
 XX
 PS Example 14; Page 47; 75pp; English.
 XX
 CC The invention relates to a targeting molecule that comprises a soluble
 CC adenoviral receptor domain, a trimerization domain and a targeting ligand
 CC domain. The targeting molecules are used for targeting an adenoviral
 CC particle to a cell expressing a cell surface molecule. The method
 CC involves contacting the adenoviral particle with the targeting molecule
 CC to form a complex, and contacting the cell with the complex, and in
 CC delivering a heterologous gene selectively to a cell. The complex is used
 CC for preparing a medicament for treatment of disease in a human mammal,
 CC such as cancer, preferably, adenocarcinoma of the prostate, by gene
 CC therapy. The present sequence represents the human coxsackie-adenovirus
 CC receptor (CAR), a 46 kDa transmembrane protein. The soluble form of CAR
 CC (sCAR) can be used in the targeting molecule of the invention.
 CC
 SO Sequence 365 AA;
 Query Match 91.1%; Score 1236; DB 23; Length 365;
 Best Local Similarity 89.3%; Pred. No. 2.6e-108;
 Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYLPCFRTLGPEDGPDIDIMWLS 60
 DB 1 MALLLCFVLLCGVADTFARSLSTTPPEMEKAGETAYLPCFRTLGPEDGPDIDIMWLS 60
 QY 61 PADNOKVDVYIIYSGDKIYDYYODLKGKRVHFTSNDLKSAGSINVTNLQSLDIGTYOC 120
 DB 61 PADNOKVDVYIIYSGDKIYDYYODLKGKRVHFTSNDLKSAGSINVTNLQSLDIGTYOC 120
 QY 121 KYKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEGDFLKCPEKGSPLPLYEMOKLSN 180
 DB 121 KYKAPGVGNKKIHLVLLVPSGRCVVDSEIEGDFLKCPEKGSPLPLYEMOKLSN 180
 QY 181 SQKLPFLMLAEMTSPIVSVKNASTEYSGTYSCTVKNRVSGDQCLRLDVVPPSNRAGTIA 240
 DB 181 SQKLPFLMLAEMTSPIVSVKNASTEYSGTYSCTVKNRVSGDQCLRLDVVPPSNRAGTIA 240
 QY 241 GAVIGVLAIVLIGLIIFCCR 261
 DB 241 GAVIGVLAIVLIGLIIFCCR 261
 RESULT 10
 AAM69698
 ID AAM69698 standard; Protein: 352 AA.
 AC AAM69698;
 XX
 DT 07-DEC-1998 (first entry)
 XX
 DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.
 XX
 KW MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
 KW Ad5 receptor; mouse; infection; vaccine; therapy.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT 35..130
 FT /note= "extracellular immunoglobulin domain"
 FT 155..220
 FT /note= "extracellular immunoglobulin domain"
 FT 45..52
 FT /note= "CVB binding region (Claim 6)"
 FT 47..51
 FT /note= "Ad2/5 and CVB binding region (Claim 6)"

FT Region 53..57
 FT /note= "Ad2/Ad5 binding region (Claim 6)"
 FT 69..73
 FT /note= "Ad2/Ad5 binding region (Claim 6)"
 FT 72..77
 FT /note= "Ad2/5 and CVB binding region (Claim 6)"
 FT 72..77
 FT /note= "CVB-binding region (Claim 6)"
 FT 77..79
 FT /note= "Ad2/Ad5 binding region (Claim 6)"
 FT 95..100
 FT /note= "CVB-binding region (Claim 6)"
 FT 122..127
 FT /note= "Ad2/5 and CVB binding region (Claim 6)"
 PN W09833819-A1.
 PD 06-AUG-1998.
 XX 30-JAN-1998; 98WO-US01724.
 PF 30-JAN-1997; 97US-0036986.
 PR (UANY) UNIT NEW YORK STATE.
 PA Philipson L, Tomko RP;
 PI
 DR WPI; 1998-437397/37.
 DR N-PSDB; AAV50430.
 XX
 XX
 PT DNA encoding human receptor for adenovirus C and coxsackievirus B -
 PT for preventing and treating viral infection and rendering cells
 PT susceptible to transformation by adenoviral vectors in gene therapy
 XX
 PS Claim 3; Page 70-71; 88pp; English.
 XX
 CC This is the amino acid sequence of mouse MCAR, a protein that
 CC serves as a cellular receptor for adenoviruses of the serotypes 2
 CC and 5 (subgroup C) and for the group B coxsackieviruses (CVB). The
 CC sequence was deduced from an isolated cDNA clone for MCAR (see
 CC AAV50430). The invention also provides host cells transformed with
 CC DNA molecules encoding MCAR or human HCAR (see AAM69697) and methods
 CC of producing the recombinant proteins or their derivatives. These
 CC proteins, their extracellular domains, as well as oligopeptides
 CC (see AAM69699-708) which bind virus, are claimed. Isolated HCAR or
 CC MCAR proteins or their fragments or variants are used to prevent or
 CC treat virus infections and for inhibiting the infectivity of Ad2,
 CC Ad5 or CVB. Methods are also provided for detecting or measuring
 CC the quantity of HCAR or MCAR in a sample, and for identifying
 CC analytes capable of binding to HCAR or MCAR.
 CC
 SO Sequence 352 AA;
 Query Match 89.5%; Score 1216; DB 19; Length 352;
 Best Local Similarity 88.1%; Pred. No. 2.9e-106;
 Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYLPCFRTLGPEDGPDIDIMWLS 60
 DB 1 MALLLCFVLLCGVADTSGITTPPEORLEKAGETAYLPCFRTLGPEDGPDIDIMWLS 60
 QY 61 PADNOKVDVYIIYSGDKIYDYYODLKGKRVHFTSNDLKSAGSINVTNLQSLDIGTYOC 120
 DB 61 PSNOKIYDVYIIYSGDKIYDNYPPDLKGRVHFTSNDVKSAGSINVTNLQSLDIGTYOC 120
 QY 121 KYKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIEGDFLKCPEKGSPLPLYEMOKLSN 180
 DB 121 KYKAPGVGNKKFLLTVLVPSGTRCFVDGSEIEGDFLKCPEKGSPLPLYEMOKLSN 180
 QY 181 SQKLPFLMLAEMTSPIVSVKNASTEYSGTYSCTVKNRVSGDQCLRLDVVPPSNRAGTIA 240
 DB 181 SQKLPFLMLAEMTSPIVSVKNASTEYSGTYSCTVKNRVSGDQCLRLDVVPPSNRAGTIA 240

QY 241 GAVIGTLALVLIGLIFCC 260
DB 241 GAVIGTLALVLIGLIFCC 260

RESULT 11

ID AAM57213 standard; Protein; 376 AA.

AC AAM57213;

DT 03-AUG-1998 (first entry)

DE Mouse coxsackievirus and adenovirus receptor.

KM Mouse; coxsackievirus; adenovirus; receptor; CAR; cardiac infection;
KM myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis;
KM pancreatic infection; acute pancreatitis; gastrointestinal tract;
KM diabetes mellitus.

OS Mus sp.

FH Key Location/Qualifiers

FT Misc-difference 366 /note="encoded by TAG, a stop codon, but the
FT sequence is shown to continue"

PN MO9811221-A2.

PD 19-MAR-1998.

PF 12-SEP-1997; 97WO-US16189.

PR 13-SEP-1996; 96US-0026100.

XX (DAND) DANA FARBER CANCER INST INC.

XX Bergelson JM, Finberg RW, Horowitz MS;

PI WPI; 1998-207384/18.

DR N-PSDB; AAV28846.

XX DNA encoding coxsackie virus and adenovirus receptor - useful for
PT modulation of e.g. cardiac, pancreatic or gastrointestinal infection

XX Disclosure; Fig 14; 104pp; English.

XX The present sequence represents mouse coxsackievirus and adenovirus
CC receptor (CAR). The present invention also describes: (1) a method for
CC modulating CAR expression comprising contacting the cell with an agent
CC which modulates CAR protein activity or CAR nucleic acid expression,
CC such that a cell associated activity is altered relative to a cell,
CC associated activity of the cell in the absence of the agent; and (2) a
CC method for detecting the presence of CAR in a biological sample
CC comprising contacting a biological sample with an agent capable of
CC detecting CAR protein or mRNA such that the presence of CAR is detected.
CC Modulation of CAR is useful for treatment of cardiac infection, e.g.
CC myocarditis, pericarditis or dilated cardiomyopathy, or infection of the
CC central nervous system, e.g. a non-specific febrile illness or
CC meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis,
CC or infection of the respiratory or gastrointestinal tract or childhood
CC onset diabetes mellitus. Probes derived from CAR nucleic acids are
CC useful for hybridisation assays, and antibodies raised against CAR
CC protein are useful for blocking CAR expression. Cell-free assays which
CC include combining CAR protein and a candidate/test compound are useful
CC in screening for drugs which interact with CAR protein.

XX Sequence 376 AA;

Query Match 89.5%; Score 1216; DB 19; Length 376;
Best Local Similarity 88.1%; Pred. No. 3.2e-106;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTSLSTTPBQMIEKAGETATVLPCEFTLCPEDQGLDIEMLLS 60
DB 1 MALLLCFVLLCGIADFTSGLSITTPBQRIEKAKGETATVLPCKFTLSPEDQGLDIEMLLS 60
QY 61 PADNOKVDPVILLYSGDKIYDDYODLKGKRVHFTNSDLKSGDASINVTNLQSDIGCTYOC 120
DB 61 PSDNOIVDPVILLYSGDKIYDNYYPDLKGRVHFTNSDLKSGDASINVTNLQSDIGCTYOC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKCPEKGSLLPLYEQKLSN 180
DB 121 KVKKAPGVANKKFLTLVLPKSGTRCFVDGSEIIGNDFLKCPEKGSLLPLYEQKLSN 180
QY 181 SQKLEPTLWLAEMTSEVYSYKNASTYSGTYSCTVKNRVSDDCLRLDVVPPSNRAGTIA 240
DB 181 SQTMPTPLWLAEMTSEVYSYKNAASSEYSGTYSCTVKNRVSDDCLRLDVVPPSNRAGTIA 240
QY 241 GAVIGTLALVLIGLIFCC 260
DB 241 GAVIGTLALVLIGLIFCC 260

RESULT 12

ID AAU83699 standard; Protein; 290 AA.

AC AAU83699;

DT 08-MAY-2002 (first entry)

DE Human PRO protein, Seq ID No 216.

KM Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KM breast cancer; prostate tumour; rectal tumour; liver tumour;
KM pericyte cell proliferation; chondrocyte cell proliferation;
KM tumour necrosis factor-alpha.

XX Homo sapiens.

XX WO200208288-A2.

XX 31-JAN-2002.

PF 29-JUN-2001; 2001WO-US21066.

XX 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.

XX (GETH) GENENTECH INC.

XX Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
DR N-PSDB; ABR33643.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11, Figure 216; 359pp; English.
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention.
 XX
 SQ Sequence 290 AA;
 Query Match 86.5%; Score 1175; DB 23; Length 290;
 Best Local Similarity 89.1%; Pred. No. 1.6e-102;
 Matches 221; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTSLSTITPEQMIKAGETAYLPQRFLLGPEDGPIIDIEWLIS 60
 DB 1 MALLLCFVLLCGVADLTSLSTITPEQMIKAGETAYLPQRFLLGPEDGPIIDIEWLIS 60
 QY 61 PADNOKVDQVYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDIGTYQC 120
 DB 61 PADNOKVDQVYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDIGTYQC 120
 QY 121 KVKKAPGVNKKIQLTVLLKPSGRCVVDGSEIIGNDFKLCPEPKESLPLLYEMOKLSN 180
 DB 121 KVKKAPGVNKKIQLTVLLKPSGRCVVDGSEIIGNDFKLCPEPKESLPLLYEMOKLSN 180
 QY 181 SQKLPFLMLAEMTSPVIVKNASTEYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
 DB 181 SQKLPFLMLAEMTSPVIVKNASTEYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
 QY 241 GAVIGVLL 248
 DB 241 GAVIGVLL 248
 QY 241 GAVIGVLL 248
 DB 241 GAVIGVLL 248
 RESULT 13
 AAW82729
 ID AAW82729 standard; Protein; 264 AA.
 XX
 AC AAW82729;
 DT 29-MAR-1999 (first entry)
 XX Adenovirus PACTSG2-SCAR protein.
 XX PACTSG2-SCAR: chimeric protein; adenoviral fibre protein; monomer;
 KM trimerisation domain; affinity; substrate; gene therapy vector;
 KM attachment; interaction assay; infection.
 XX Mastadenovirus.
 OS Synthetic.
 XX WO9854346-A1.
 XX PD 03-DEC-1998.
 XX

PF 28-MAY-1998; 98WO-US11024.
 XX 16-JAN-1998; 98US-0071668.
 PR 28-MAY-1997; 97US-0047849.
 XX (GENV-) GENVEC INC.
 XX Brough DE, Einfeld D, Kovessi I, Lizonova A, Reivink PW;
 PI Wickham TJ, Yonehiro G;
 XX WPI: 1999-059848/05.
 DR N-PSDB; AAV72025.
 XX New adenoviral fibre trimer with reduced binding to native substrate
 PT - useful for, e.g. preparing gene therapy vector with minimal
 PT ectopic infection for in vitro applications
 PS Example 8; Page 58-59; 103pp; English.
 XX This sequence represents a novel adenovirus chimeric protein,
 CC PACTSG2-SCAR. This protein is used in a method for the construction of
 CC novel monomers having an N-terminus of an adenoviral fibre protein and
 CC a trimerisation domain. Such monomers have lower affinity for native
 CC substrate than the native adenoviral fibre trimer. Cell lines containing
 CC such monomers are used (i) to propagate adenoviruses for use as gene
 CC therapy vectors (for in vitro or in vivo applications), (ii) as reagents
 CC for studying adenoviral attachment and infection, and (iii) in
 CC receptor-ligand interaction assays. The new viruses produce minimal
 CC ectopic infection (they can not infect native host cells) so are safer as
 CC vectors and can be engineered for selective targeting to other cells.
 XX
 SQ Sequence 264 AA;
 Query Match 84.0%; Score 1142; DB 20; Length 264;
 Best Local Similarity 88.4%; Pred. No. 1.9e-99;
 Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MALLLCFVLLCGVADLTSLSTITPEQMIKAGETAYLPQRFLLGPEDGPIIDIEWLIS 60
 DB 1 MALLLCFVLLCGVADLTSLSTITPEQMIKAGETAYLPQRFLLGPEDGPIIDIEWLIS 60
 QY 61 PADNOKVDQVYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDIGTYQC 120
 DB 61 PADNOKVDQVYIILYSGDKIYDDYQDLKGRVHTSNDLKSGDASINVTNLQSLDIGTYQC 120
 QY 121 KVKKAPGVNKKIQLTVLLKPSGRCVVDGSEIIGNDFKLCPEPKESLPLLYEMOKLSN 180
 DB 121 KVKKAPGVNKKIQLTVLLKPSGRCVVDGSEIIGNDFKLCPEPKESLPLLYEMOKLSN 180
 QY 181 SQKLPFLMLAEMTSPVIVKNASTEYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
 DB 181 SQKLPFLMLAEMTSPVIVKNASTEYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
 QY 241 GA 242
 DB 241 GS 242
 QY 241 GA 242
 DB 241 GS 242
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 AAW82730
 ID AAW82730 standard; Protein; 277 AA.
 XX
 AC AAW82730;
 DT 29-MAR-1999 (first entry)
 XX Adenovirus SCAR.RGD protein.
 XX SCAR.RGD: chimeric protein; adenoviral fibre protein; monomer;
 KM trimerisation domain; affinity; substrate; gene therapy vector;
 KM attachment; interaction assay; infection.
 XX Mastadenovirus.
 OS

```

OS Synthetic.
XX WO9854346-A1.
XX 03-DEC-1998.
XX
XX 28-MAY-1998; 98WO-US11024.
XX
XX 16-JAN-1998; 98US-0071668.
XX 28-MAY-1997; 97US-0047849.
XX
XX (GENV-) GENVEC INC.
XX
XX Brough DE, Einfeld D, Kovesdi I, Lizonova A, Roelvink PW;
XX Wickham TJ, Yonehiro G;
XX
XX WPI: 1999-059848/05.
XX N-PSDB; AAV72026.
XX
XX
XX PT New adenoviral fibre trimer with reduced binding to native substrate
XX PT - useful for, e.g. preparing gene therapy vector with minimal
XX PT ectopic infection for in vitro applications
XX
XX PS Example 8; Page 59-60; 103pp; English.
XX
XX CC This sequence represents a novel adenovirus chimeric protein, SCAR.RGD.
XX CC This protein is used in a method for the construction of novel monomers
XX CC having an N-terminus of an adenoviral fibre protein and a trimerisation
XX CC domain. Such monomers have lower affinity for native substrate than the
XX CC native adenoviral fibre trimer. Cell lines containing such monomers are
XX CC used (i) to propagate adenovirus for use as gene therapy vectors (for in
XX CC vitro or in vivo applications, (ii) as reagents for studying adenoviral
XX CC attachment and infection, and (iii) in receptor-ligand interaction
XX CC assays. The new viruses produce minimal ectopic infection (they can not
XX CC infect native host cells) so are safer as vectors and can be engineered
XX CC for selective targeting to other cells.
XX
XX SQ Sequence 277 AA;
XX
XX Query Match 84.0%; Score 1142; DB 20; Length 277;
XX Best Local Similarity 88.4%; Pred. No. 2e-99;
XX Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
XX
XX QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYLPCRFLLGPEDOGPIIDIEMLLS 60
XX 1 MALLLCFVLLCGVADPARSLSTTPPEOMTEKAGETAYLPCRFLLGPEDOGPIIDIEMLLS 60
XX
XX Db 61 PADNOKVDQVILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
XX 61 PADNOKVDQVILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
XX
XX QY 121 KYKKAQGVGNKKIQLTVLLKPSGTRCYVDSSEIIGDFLKEPKEGSLPLQYEWOKLSD 180
XX 121 KYKKAQGVGNKKIHLVLLVPSGARCYVDSSEIIGDFLKEPKEGSLPLQYEWOKLSD 180
XX
XX Db 181 SQKLPFLMLAEMTSPVIVKNASTEYSGTCTVKRVGSDQCLRLDVPVPSNRAGTIA 240
XX 181 SQKLPFLMLAEMTSPVIVKNASTEYSGTCTVKRVGSDQCLRLDVPVPSNRAGTIA 240
XX
XX QY 241 GA 242
XX 241 GA 242
XX
XX Db 241 GS 242
XX
XX
XX RESULT 15
XX AAW82731
XX ID AAW82731 standard; Protein; 397 AA.
XX
XX AC AAW82731;
XX
XX XX
XX DT 29-MAR-1999 (first entry)
XX
XX DE Adenovirus PACSG2SCAR.slg chimeric protein.

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XX XX
XX PACSG2SCAR.slgDEL; chimeric protein; adenoviral fibre protein;
XX trimerisation domain; affinity; substrate; gene therapy vector;
XX infection; attachment; interaction assay; vector; monomer.
XX
XX OS Mastadenovirus.
XX OS Synthetic.
XX
XX PN WO9854346-A1.
XX
XX 03-DEC-1998.
XX
XX 28-MAY-1998; 98WO-US11024.
XX
XX 16-JAN-1998; 98US-0071668.
XX 28-MAY-1997; 97US-0047849.
XX
XX (GENV-) GENVEC INC.
XX
XX Brough DE, Einfeld D, Kovesdi I, Lizonova A, Roelvink PW;
XX Wickham TJ, Yonehiro G;
XX
XX WPI: 1999-059848/05.
XX N-PSDB; AAV72027.
XX
XX
XX PT New adenoviral fibre trimer with reduced binding to native substrate
XX PT - useful for, e.g. preparing gene therapy vector with minimal
XX PT ectopic infection for in vitro applications
XX
XX PS Example 10; Page 60-62; 103pp; English.
XX
XX CC This sequence represents a novel adenovirus chimeric protein,
XX CC PACSG2SCAR.slgDEL. This protein is used in a method for the
XX CC construction of novel monomers having an N-terminus of an adenoviral
XX CC fibre protein and a trimerisation domain. Such monomers have lower
XX CC affinity for native substrate than the native adenoviral fibre trimer.
XX CC Cell lines containing such monomers are used (i) to propagate adenovirus
XX CC for use as gene therapy vectors (for in vitro or in vivo applications,
XX CC (ii) as reagents for studying adenoviral attachment and infection, and
XX CC (iii) in receptor-ligand interaction assays. The new viruses produce
XX CC minimal ectopic infection (they can not infect native host cells) so are
XX CC safer as vectors and can be engineered for selective targeting to other
XX CC cells.
XX
XX SQ Sequence 397 AA;
XX
XX Query Match 84.0%; Score 1142; DB 20; Length 397;
XX Best Local Similarity 88.4%; Pred. No. 3.4e-99;
XX Matches 214; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
XX
XX QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMTEKAGETAYLPCRFLLGPEDOGPIIDIEMLLS 60
XX 1 MALLLCFVLLCGVADPARSLSTTPPEOMTEKAGETAYLPCRFLLGPEDOGPIIDIEMLLS 60
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XX Db 61 PADNOKVDQVILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
XX 61 PADNOKVDQVILYSGDKIYDDYODLKGKRVHFTSNDLSKGASINVTNLQSLDICTYOC 120
XX
XX QY 121 KYKKAQGVGNKKIQLTVLLKPSGTRCYVDSSEIIGDFLKEPKEGSLPLQYEWOKLSD 180
XX 121 KYKKAQGVGNKKIHLVLLVPSGARCYVDSSEIIGDFLKEPKEGSLPLQYEWOKLSD 180
XX
XX Db 181 SQKLPFLMLAEMTSPVIVKNASTEYSGTCTVKRVGSDQCLRLDVPVPSNRAGTIA 240
XX 181 SQKLPFLMLAEMTSPVIVKNASTEYSGTCTVKRVGSDQCLRLDVPVPSNRAGTIA 240
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XX QY 241 GA 242
XX 241 GA 242
XX
XX Db 241 GS 242
XX
XX
XX Search completed: July 9, 2003, 12:44:32
XX Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:43:53 ; Search time 14 Seconds

(without alignments)
548.527 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359
Sequence: 1 MALLICFVLLCGVADLTSL.....AVIGVLLALVLLIGLIFCCR 261Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 1238 | 91.1 | 365 | 2 | US-08-979-424-3 |
| 2 | 1238 | 91.1 | 365 | 4 | US-09-272-496-2 |
| 3 | 1224 | 90.1 | 365 | 4 | US-08-928-3838-2 |
| 4 | 1217 | 89.6 | 365 | 4 | US-08-928-3838-23 |
| 5 | 1217 | 89.6 | 365 | 4 | US-08-928-3838-24 |
| 6 | 1216 | 89.5 | 365 | 4 | US-08-928-3838-26 |
| 7 | 523 | 38.5 | 106 | 4 | US-08-928-3838-8 |
| 8 | 453 | 33.3 | 95 | 4 | US-08-928-3838-17 |
| 9 | 351.5 | 25.9 | 273 | 4 | US-09-254-465A-26 |
| 10 | 351.5 | 25.9 | 319 | 1 | US-08-597-4958-22 |
| 11 | 351.5 | 25.9 | 319 | 4 | US-09-068-051A-22 |
| 12 | 351.5 | 25.9 | 319 | 4 | US-09-336-536-67 |
| 13 | 351.5 | 25.9 | 319 | 4 | US-09-254-465A-6 |
| 14 | 341.5 | 23.2 | 270 | 4 | US-09-254-465A-32 |
| 15 | 315.5 | 23.2 | 318 | 4 | US-09-068-051A-32 |
| 16 | 258 | 19.0 | 387 | 4 | US-09-175-928-2 |
| 17 | 246.5 | 18.1 | 394 | 4 | US-09-336-536-39 |
| 18 | 244 | 18.0 | 365 | 4 | US-09-336-536-40 |
| 19 | 217 | 16.0 | 390 | 2 | US-08-979-424-1 |
| 20 | 199.5 | 14.7 | 249 | 4 | US-09-336-536-42 |
| 21 | 196 | 14.4 | 299 | 4 | US-09-188-930-331 |
| 22 | 196 | 14.4 | 299 | 4 | US-09-462-270-2 |
| 23 | 196 | 14.4 | 299 | 4 | US-09-254-465A-1 |
| 24 | 191 | 14.1 | 299 | 4 | US-09-188-930-189 |
| 25 | 190 | 14.0 | 370 | 4 | US-09-336-536-28 |
| 26 | 189 | 13.9 | 341 | 4 | US-09-336-536-29 |
| 27 | 184 | 13.5 | 263 | 4 | US-09-254-465A-25 |

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|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 181.5 | 13.4 | 312 | 4 | US-09-254-465A-9 | Sequence 9, Appl |
| 29 | 180 | 13.2 | 260 | 4 | US-09-254-465A-23 | Sequence 23, Appl |
| 30 | 178.5 | 13.1 | 298 | 4 | US-09-152-060-76 | Sequence 76, Appl |
| 31 | 163.5 | 12.0 | 321 | 4 | US-09-254-465A-2 | Sequence 2, Appl |
| 32 | 163 | 12.0 | 246 | 4 | US-09-336-536-31 | Sequence 31, Appl |
| 33 | 161.5 | 11.9 | 300 | 4 | US-09-254-465A-10 | Sequence 10, Appl |
| 34 | 158 | 11.6 | 209 | 4 | US-09-430-503-20 | Sequence 20, Appl |
| 35 | 158 | 11.6 | 209 | 4 | US-09-430-503-24 | Sequence 24, Appl |
| 36 | 156 | 11.5 | 209 | 4 | US-09-430-503-18 | Sequence 18, Appl |
| 37 | 156 | 11.5 | 209 | 4 | US-09-430-503-22 | Sequence 22, Appl |
| 38 | 155 | 11.4 | 269 | 4 | US-09-430-503-4 | Sequence 4, Appl |
| 39 | 155 | 11.4 | 269 | 4 | US-09-430-503-6 | Sequence 6, Appl |
| 40 | 155 | 11.4 | 269 | 4 | US-09-430-503-8 | Sequence 8, Appl |
| 41 | 154 | 11.3 | 306 | 4 | US-08-205-697A-17 | Sequence 17, Appl |
| 42 | 154 | 11.3 | 306 | 4 | US-08-702-525-17 | Sequence 17, Appl |
| 43 | 154 | 11.3 | 306 | 4 | US-09-651-2007-17 | Sequence 17, Appl |
| 44 | 154 | 11.3 | 306 | 5 | PCT-US95-02576-17 | Sequence 17, Appl |
| 45 | 153 | 11.3 | 269 | 4 | US-09-430-503-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-979-424-3
; Sequence 3, Application US/08979424
; Patent No. 5942606
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,424
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0405 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1946351
; US-08-979-424-3
Query Match 91.1%; Score 1238; DB 2; Length 365;
Best Local Similarity 89.3%; Pred. No. 1e-114;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMIEKAGETAYLPCKFTLGEEDGPIIDIEWLLS 60
1 MALLLCFVLLCGVADFPARSLSTTPPEOMIEKAGETAYLPCKFTLSPEDGPIIDIEWLLS 60
Db 61 PADNOKVDDVITILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
121 KYKKAAGVGNKKIQLTVLKPSTGRCYVDGSEIINDFKLCEPKESGLPLIYEMOKLSN 180
Db 61 PADNOKVDDVITILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
121 KYKKAAGVGNKKIQLTVLKPSTGRCYVDGSEIINDFKLCEPKESGLPLIYEMOKLSN 180
QY 181 SQKPLTFLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
181 SQKPLTFLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
Db 241 GAVIGVLALVLIIGLIIFCCR 261
241 GAVIGVLALVLIIGLIIFCCR 261

RESULT 2

US-09-272-496-2
Sequence 2, Application US/09272496
Patent No. 6245966
GENERAL INFORMATION:
APPLICANT: Degregori, James
TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
FILE REFERENCE: 90-98
CURRENT APPLICATION NUMBER: US/09/272,496
CURRENT FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/092782
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-09-272-496-2

Query Match 91.1%; Score 1238; DB 4; Length 365;
Best Local Similarity 89.3%; Pred. NO. 1e-114;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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1 MALLLCFVLLCGVADFPARSLSTTPPEOMIEKAGETAYLPCKFTLSPEDGPIIDIEWLLS 60
Db 61 PADNOKVDDVITILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
121 KYKKAAGVGNKKIQLTVLKPSTGRCYVDGSEIINDFKLCEPKESGLPLIYEMOKLSN 180
Db 61 PADNOKVDDVITILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
121 KYKKAAGVGNKKIQLTVLKPSTGRCYVDGSEIINDFKLCEPKESGLPLIYEMOKLSN 180
QY 181 SQKPLTFLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
181 SQKPLTFLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
Db 241 GAVIGVLALVLIIGLIIFCCR 261
241 GAVIGVLALVLIIGLIIFCCR 261

RESULT 3

US-08-928-383B-2
Sequence 2, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,

APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandagouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-383B-2

Query Match 90.1%; Score 1224; DB 4; Length 365;
Best Local Similarity 88.9%; Pred. NO. 2.5e-113;
Matches 232; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLSTTPPEOMIEKAGETAYLPCKFTLGEEDGPIIDIEWLLS 60
1 MALLLCFVLLCGVADFPARSLSTTPPEOMIEKAGETAYLPCKFTLSPEDGPIIDIEWLLS 60
Db 61 PADNOKVDDVITILYSGDKIYDDYODLKGKRVHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
121 KYKKAAGVGNKKIQLTVLKPSTGRCYVDGSEIINDFKLCEPKESGLPLIYEMOKLSN 180
Db 121 KYKKAAGVGNKKIQLTVLKPSTGRCYVDGSEIINDFKLCEPKESGLPLIYEMOKLSN 180
QY 181 SQKPLTFLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
181 SQKPLTFLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDOCLRLDVVPPSNRAGTIA 240
Db 241 GAVIGVLALVLIIGLIIFCCR 261
241 GAVIGVLALVLIIGLIIFCCR 261

RESULT 4

US-08-928-383B-23
Sequence 23, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/928,383B
;; FILING DATE: 12-SEP-1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/026,100
;; FILING DATE: 13-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: DFN-020
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 365 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;;
;; US-08-928-383B-23

Query Match 89.6%; Score 1217; DB 4; Length 365;
Best Local Similarity 88.1%; Pred. No. 1.2e-112;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

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DB 1 MARLLCFVLLCGIADFTSGISITTPBQRIEKAKEGTAYLPCKFTLSPEDOGPLDIEMWLS 60
QY 61 PADNOKVQDVIILYSGDKIYDYYODLKGKRVHFTSNDLKSAGASINVTNLQSLDICTYOC 120
DB 61 PSNNOIVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVSGASINVTNLQSLDICTYOC 120
QY 121 KYKKAAGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKCPEKESLPLLEYMOKLSN 180
DB 121 KYKKAAGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKCPEKESLPLLEYMOKLSN 180
QY 181 SOKLPTLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
DB 181 SOTMPTSLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGVLLALVLIGLIIFCC 260
DB 241 GAVIGVLLALVLIGLIIFCC 260
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RESULT 5

US-08-928-383B-24
; Sequence 24, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/928,383B
;; FILING DATE: 12-SEP-1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/026,100
;; FILING DATE: 13-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: DFN-020
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 365 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;;
;; US-08-928-383B-24

Query Match 89.6%; Score 1217; DB 4; Length 365;
Best Local Similarity 88.1%; Pred. No. 1.2e-112;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

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QY 1 MALLLCFVLLCGVADLTSLISITTPBOMTEKAGETAYLPCTRFTLSPEDOGPLDIEMWLS 60
DB 1 MARLLCFVLLCGIADFTSGISITTPBQRIEKAKEGTAYLPCKFTLSPEDOGPLDIEMWLS 60
QY 61 PADNOKVQDVIILYSGDKIYDYYODLKGKRVHFTSNDLKSAGASINVTNLQSLDICTYOC 120
DB 61 PSNNOIVDQVILYSGDKIYDNYYPDLKGRVHFTSNDVSGASINVTNLQSLDICTYOC 120
QY 121 KYKKAAGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKCPEKESLPLLEYMOKLSN 180
DB 121 KYKKAAGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFLKCPEKESLPLLEYMOKLSN 180
QY 181 SOKLPTLWLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
DB 181 SOTMPTSLAEMTSPVIVKNASTEYSGTYSCTVKNRVGSDQCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGVLLALVLIGLIIFCC 260
DB 241 GAVIGVLLALVLIGLIIFCC 260
```

RESULT 6

US-08-928-383B-26
; Sequence 26, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-383B-26

Query Match 89.5%; Score 1216; DB 4; Length 365;
Best Local Similarity 88.1%; Pred. No. 1.6e-112;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLFGVLLCGVADITRSLSITTPPEQMEKAGETAYLPCRFLLGPEDEGPDIDIELLS 60
DB 1 MALLLFGVLLCGVADITRSLSITTPPEQMEKAGETAYLPCRFLLGPEDEGPDIDIELLS 60
QY 61 PADNQRVDQVYIILYSGDKIYDDYQDLKGRHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
DB 61 PSBNQIVDQVYIILYSGDKIYDDYQDLKGRHFTSNDLKSGDASINVTNLQSLDIGTYQC 120
QY 121 KYKAGVGNKKIQLVTLKPSGTRCVGSEIEIINDFKLCKPKKGSPLLYEMOKLSN 180
DB 121 KYKAGVGNKKIQLVTLKPSGTRCVGSEIEIINDFKLCKPKKGSPLLYEMOKLSN 180
QY 181 SGLPLTLMIAEMTSPIYVSNQASTEXSGTSCVKNRVGSDQCLLRDLVVPENRAGTIA 240
DB 181 SGLPLTLMIAEMTSPIYVSNQASTEXSGTSCVKNRVGSDQCLLRDLVVPENRAGTIA 240
QY 241 GAVIGVLLALVILGLIIFCC 260
DB 241 GAVIGVLLALVILGLIIFCC 260

RESULT 7
US-08-928-383B-8
Sequence 8, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-928-383B-8

Query Match 38.5%; Score 523; DB 4; Length 106;
Best Local Similarity 92.5%; Pred. No. 1.4e-44;
Matches 98; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 34 GETAYLPCRFLLGPEDEGPDIDIELLSPADNQRVDQVYIILYSGDKIYDDYQDLKGRVHF 93
DB 1 GETAYLPCRFLLGPEDEGPDIDIELLSPADNQRVDQVYIILYSGDKIYDDYQDLKGRVHF 93
QY 94 TSNDLKS GDASINVTNLQSLDIGTYQCKVKKAPGVGNKKIQLVTL 139
DB 61 TSNDLKS GDASINVTNLQSLDIGTYQCKVKKAPGVGNKKIHLVTLV 106

RESULT 8
US-08-928-383B-17
Sequence 17, Application US/08928383B
Patent No. 6210921
GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
APPLICANT: and Marshall S. Horwitz
TITLE OF INVENTION: CAR, A No. 6210921e1 Coxsackievirus and Adenovirus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 6
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-6

Query Match 25.9%; Score 351.5; DB 4; Length 319;
Best Local Similarity 34.1%; Pred. No. 7.3e-27;
Matches 89; Conservative 53; Mismatches 96; Indels 23; Gaps 11;

QY 10 LCGVADLTSLSTTPEQMIEKAGETAYLPCRFTLGPEDGPIDIEM---LISPADNOK 66
DB 12 LCAVRYTVDAISVETPODVLRAISGKSVLPCYHSTSSREGL-IQMDKLLT-----H 65
QY 67 VQOVITLISGDK--ITDDYVQDLKGRVHFTSNDLKSGDASINVTNLQSLDIGYQCKVK 124
DB 66 TERVITWPSNKNYHIGELY---KNRVSI-SNNAEQSDASITIDQLTMADNGTECSVSL 121
QY 125 AGCV-GNKK--IQLTVLKPSGTCRYVDGSEIIGNDFKLKCEPKESLPLLYEMOKLS-N 180
DB 122 MSDLESGNTSKRVLLVLPSPKCEGIEGTTIGNNIQLTCQKESGPTPOYSWKRYNLL 181
QY 181 SOKLPTLMLAEMTS-PVISVKNASTESGTCYVKNRVGSDQCLRLDVPPSNRAGTI 239
DB 182 NQEQP---LAQPSAGPVLKNIKISTDTSGYICTSSNEGTCPCNTTAVRSRSMVALY 238
QY 240 AGAVIGVLLALVLIIGLIIFCC 260
DB 239 VGIAVGVAALLIIGIIYYCC 259

RESULT 14
US-09-254-465A-24
Sequence 24, Application US/09254465A
Patent No. 6410708
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Napier, Mary A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
FILE REFERENCE: P1216R1 (US)
CURRENT APPLICATION NUMBER: US/09/254,465A
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: US 60/066,364
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 60/078,936
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/19437
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 24
LENGTH: 270
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-465A-24

Query Match 25.1%; Score 341.5; DB 4; Length 270;
Best Local Similarity 34.1%; Pred. No. 5.6e-26;
Matches 86; Conservative 53; Mismatches 90; Indels 23; Gaps 11;
QY 19 SLSTTPEQMIEKAGETAYLPCRFTLGPEDGPIDIEM---LISPADNOKVQVITLIS 75

DB 7 A1SVETPODVLRAISGKSVLPCYHSTSSREGL-IQMDKLLT-----HTEVITWPF 60
QY 76 GDK--IYDDYQDLKGRVHFTSNDLKSGDASINVTNLQSLDIGYQCKVKKAPGV-GNKK 132
DB 61 SKNYIHGELY---KNRVSI-SNNAEQSDASITIDQLTMADNGTECSVSLSDLEGNTK 116
QY 133 --IQLTVLKPSGTCRYVDGSEIIGNDFKLKCEPKESLPLLYEMOKLS-NSQKLPITLW 189
DB 117 SVRLVLVLPSPKCEGIEGTTIGNNIQLTCQKESGPTPOYSWKRYNLLNDEQP---L 173
QY 190 AEMTS-PVISVKNASTESGTCYVKNRVGSDQCLRLDVPPSNRAGTIAGAVIGVLL 248
DB 174 AQPASGQPVSLKNIKISTDTSGYICTSSNEGTCPCNTTAVRSRSMVALYVGIAVGVA 233
QY 249 ALVIGLIIFCC 260
DB 234 ALIIGIIYYCC 245

RESULT 15
US-09-068-051A-32
Sequence 32, Application US/09068051A
Patent No. 6291235
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritzer, Gerd;
Simpson, Richard J.; Nice, Edward; Moritz, R. L.;
Carmel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,495
FILING DATE: 02-Feb-1996
APPLICATION NUMBER: 08/511,876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6291235man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5316.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-068-051A-32

Query Match 23.2%; Score 315.5; DB 4; Length 318;
Best Local Similarity 30.7%; Pred. No. 2.7e-23;
Matches 81; Conservative 50; Mismatches 106; Indels 27; Gaps 10;
QY 9 LCGVADLTSLSTTPEQMIEKAGETAYLPCRFTLGPEDGPIDIEM---LISPADNOK 66

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:44:38 ; Search time 23 Seconds
(without alignments)
1321.111 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359
Sequence: 1 MALLLCEVLLCGVADITRSL.....AVIGVLLALVIGLIIFCCR 261

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/PCT05_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubppaa/US05_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 1359 | 100.0 | 261 | 10 US-09-899-634A-2 | Sequence 2, Appl |
| 2 | 1353 | 99.6 | 365 | 10 US-09-899-634A-4 | Sequence 4, Appl |
| 3 | 1238 | 91.1 | 352 | 9 US-09-992-598-505 | Sequence 505, App |
| 4 | 1238 | 91.1 | 352 | 9 US-09-989-293A-505 | Sequence 505, App |
| 5 | 1238 | 91.1 | 352 | 9 US-09-989-735-505 | Sequence 505, App |
| 6 | 1238 | 91.1 | 352 | 9 US-09-990-444-505 | Sequence 505, App |
| 7 | 1238 | 91.1 | 352 | 9 US-10-053-107-10 | Sequence 10, Appl |
| 8 | 1238 | 91.1 | 352 | 9 US-09-989-730-505 | Sequence 505, App |
| 9 | 1238 | 91.1 | 352 | 9 US-09-990-436-505 | Sequence 505, App |
| 10 | 1238 | 91.1 | 352 | 9 US-09-991-181-505 | Sequence 505, App |
| 11 | 1238 | 91.1 | 352 | 9 US-09-993-687-505 | Sequence 505, App |
| 12 | 1238 | 91.1 | 352 | 9 US-09-989-734-505 | Sequence 505, App |
| 13 | 1238 | 91.1 | 352 | 9 US-09-997-653-505 | Sequence 505, App |
| 14 | 1238 | 91.1 | 352 | 9 US-09-993-667-505 | Sequence 505, App |
| 15 | 1238 | 91.1 | 352 | 9 US-09-990-438-505 | Sequence 505, App |
| 16 | 1238 | 91.1 | 352 | 9 US-09-990-562-505 | Sequence 505, App |
| 17 | 1238 | 91.1 | 352 | 9 US-09-997-428-505 | Sequence 505, App |
| 18 | 1238 | 91.1 | 352 | 9 US-09-997-666-505 | Sequence 505, App |
| 19 | 1238 | 91.1 | 352 | 9 US-10-227-884-216 | Sequence 216, App |

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| 20 | 1238 | 91.1 | 352 | 9 US-09-990-711-505 | Sequence 505, App |
| 21 | 1238 | 91.1 | 352 | 9 US-10-230-163-216 | Sequence 216, App |
| 22 | 1238 | 91.1 | 352 | 9 US-09-989-726-505 | Sequence 505, App |
| 23 | 1238 | 91.1 | 352 | 9 US-09-990-437-505 | Sequence 505, App |
| 24 | 1238 | 91.1 | 352 | 9 US-09-998-156-505 | Sequence 505, App |
| 25 | 1238 | 91.1 | 352 | 9 US-10-218-631-216 | Sequence 216, App |
| 26 | 1238 | 91.1 | 352 | 9 US-10-230-338-216 | Sequence 216, App |
| 27 | 1238 | 91.1 | 352 | 9 US-09-991-157-505 | Sequence 505, App |
| 28 | 1238 | 91.1 | 352 | 9 US-09-991-172-505 | Sequence 505, App |
| 29 | 1238 | 91.1 | 352 | 9 US-09-997-514-505 | Sequence 505, App |
| 30 | 1238 | 91.1 | 352 | 9 US-09-997-573-505 | Sequence 505, App |
| 31 | 1238 | 91.1 | 352 | 9 US-10-230-414-216 | Sequence 216, App |
| 32 | 1238 | 91.1 | 352 | 9 US-09-990-443-505 | Sequence 505, App |
| 33 | 1238 | 91.1 | 352 | 9 US-09-990-726-505 | Sequence 505, App |
| 34 | 1238 | 91.1 | 352 | 9 US-09-997-559-505 | Sequence 505, App |
| 35 | 1238 | 91.1 | 352 | 9 US-09-997-601-505 | Sequence 505, App |
| 36 | 1238 | 91.1 | 352 | 9 US-09-989-729A-505 | Sequence 505, App |
| 37 | 1238 | 91.1 | 352 | 9 US-09-990-440-505 | Sequence 505, App |
| 38 | 1238 | 91.1 | 352 | 9 US-09-991-854-505 | Sequence 505, App |
| 39 | 1238 | 91.1 | 352 | 9 US-09-997-349-505 | Sequence 505, App |
| 40 | 1238 | 91.1 | 352 | 9 US-09-997-440-505 | Sequence 505, App |
| 41 | 1238 | 91.1 | 352 | 9 US-09-997-628-505 | Sequence 505, App |
| 42 | 1238 | 91.1 | 352 | 9 US-09-997-683-505 | Sequence 505, App |
| 43 | 1238 | 91.1 | 352 | 9 US-10-213-145-10 | Sequence 10, Appl |
| 44 | 1238 | 91.1 | 352 | 9 US-09-993-463-505 | Sequence 505, App |
| 45 | 1238 | 91.1 | 352 | 9 US-09-993-748-505 | Sequence 505, App |

ALIGNMENTS

RESULT 1
US-09-899-634A-2
; Sequence 2, Application US//0989634A
; Patent No. US2002059654A1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gadiant, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: PCAR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899, 634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: porcine
US-09-899-634A-2

Query Match 100.0%; Score 1359; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 4.5e-89;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MALLLCEVLLCGVADITRSLSTTPPEOMIEKAGETAYVPCFFLAGPEDQGLDIEMWLS | 60 |
| DB | 1 | MALLLCEVLLCGVADITRSLSTTPPEOMIEKAGETAYVPCFFLAGPEDQGLDIEMWLS | 60 |
| QY | 61 | PADNOKVDDVITLLVSGDKYDDYDYLKGRVFTSNDLKSASINVTNLQSDIGTYOC | 120 |
| DB | 61 | PADNOKVDDVITLLVSGDKYDDYDYLKGRVFTSNDLKSASINVTNLQSDIGTYOC | 120 |
| QY | 121 | KYKKAAGVGNKKIQTLVLLKPSGTRCYVDGSEIENDFLKCEPEEGSLPLLEYMOXLN | 180 |
| DB | 121 | KYKKAAGVGNKKIQTLVLLKPSGTRCYVDGSEIENDFLKCEPEEGSLPLLEYMOXLN | 180 |
| QY | 181 | SKQLPTLWLAEMTSPVIVKNASTEVSGTCTVXNRVSGDCLRLDVPVPSNRAGTIA | 240 |
| DB | 181 | SKQLPTLWLAEMTSPVIVKNASTEVSGTCTVXNRVSGDCLRLDVPVPSNRAGTIA | 240 |
| QY | 241 | GAVIGVLLALVIGLIIFCCR 261 | |
| DB | 241 | GAVIGVLLALVIGLIIFCCR 261 | |

RESULT 2
US-09-899-634A-4
; Sequence 4, Application US/09899634A
; Patent No. US20020059654A1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gadient, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: pCAR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899,634A
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 365
; TYPE: PRT
; ORGANISM: porcine
US-09-899-634A-4

Query Match 99.6%; Score 1353; DB 10; Length 365;
Best Local Similarity 99.6%; Pred. No. 1,7e-88;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLCFVLLCGVADLTRSLSTTPPEOMIEKAGETAYLPQRFLLGPEDDGPDIDIEWLIS 60
DB 1 MALLCFVLLCGVADLTRSLSTTPPEOMIEKAGETAYLPQRFLLGPEDDGPDIDIEWLIS 60
QY 61 PADNOKVDQVYIIYSGDKIYDDYODLKGKRVHFTSNDLKSQDASINVTNLQSLDIGYQC 120
DB 61 PADNOKVDQVYIIYSGDKIYDDYODLKGKRVHFTSNDLKSQDASINVTNLQSLDIGYQC 120
QY 121 KVKKAPGVGNKKIQLTVLKPSGTRCYVDSSEIIGNDFKLCKEKEGSLPLYLEWQKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLKPSGTRCYVDSSEIIGNDFKLCKEKEGSLPLYLEWQKLSN 180
QY 181 SOKLPTLMALMTSPVSVKNASTEGTISCTYKRVNRYGSDQCLLRDVPVPSNRAGTIA 240
DB 181 SOKLPTLMALMTSPVSVKNASTEGTISCTYKRVNRYGSDQCLLRDVPVPSNRAGTIA 240
QY 241 GAVIGVLLALVLLGLIIFCC 260
DB 241 GAVIGVLLALVLLGLIIFCC 260

RESULT 3
US-09-992-598-505
; Sequence 505, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC20
;; CURRENT APPLICATION NUMBER: US/09/992,598
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MALLLCFVLLCGVALTSSLSITTEPQMIERAKGETAVLPCEFTGPEPDGPILEWLIS 60
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Qy 121 KYKKAPEGVGNKKIQLTVLTKPSGTRCYVDGSEIENDFKLCEPEGSLPLLYEQKLSN 180
Db 121 KYKKAPEGVGNKKIHVLVVKPSGARCVDGSEIENDFKLCEPEGSLPLLYEQKLSN 180

Qy 181 SGLPTLWLAEMTSVIVSKNASTESGYSCTVKNRVGSDQCLRLDVPPSNRAGTIA 240
Db 181 SGLPTLWLAEMTSVIVSKNASTESGYSCTVKNRVGSDQCLRLDVPPSNRAGTIA 240

Qy 241 GAVIGVLLALVYLGLIFCCR 261
Db 241 GAVIGVLLALVYLGLIFCCR 261

RESULT 4
US-09-989-293A-505
; Sequence 505, Application US/09989293A
; Patent No. US2002017164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
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Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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DB 121 KYKAGVGNKKIQLTVLTKPSGTRCYVDGSEIEGNDPFLKCEPKKESLPLLEYMOKLSN 180
QY 181 SQKLPFLMLAEMTSPIVSVKNASTESGYTSCVTKRVSGDGLRLDVPVPSNRAQTIA 240
DB 181 SQKLPFLMLAEMTSPIVSVKNASTESGYTSCVTKRVSGDGLRLDVPVPSNRAQTIA 240
QY 241 GAVIGVLLALVGLIIFCCR 261
DB 241 GAVIGVLLALVGLIIFCCR 261

RESULT 5
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; Sequence 505, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman
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;; APPLICANT: Goddard, Audrey
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;; APPLICANT: Stewart, Timothy A.
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;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C61
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MLLLCFVLLCGVADLTRELSITTPPEOMTERAKGETAYLPCRFITGPEDOGFLDIEMULS 60
DB 1 MLLLCFVLLCGVADLTRELSITTPPEOMTERAKGETAYLPCRFITGPEDOGFLDIEMULS 60
QY 61 PADNOKVDPVILLYSGDKIYDDYODLKGKRVHFTSNDLSKSGDASINVTNLQUSDIGTYOC 120
DB 61 PADNOKVDPVILLYSGDKIYDDYODLKGKRVHFTSNDLSKSGDASINVTNLQUSDIGTYOC 120
QY 121 KYKAPGVGNKKIQLTVLTKPSGTRCYVDGSEIEIGNDFLKEPBGSLPLLYEWOXLSN 180
DB 121 KYKAPGVGNKKIQLTVLTKPSGTRCYVDGSEIEIGNDFLKEPBGSLPLLYEWOXLSN 180
QY 181 SOKLPTMLAEMTSPVIVKRNASTYSGTGVKRNRYGSDOCLRLDVPVPPSNRAGTIA 240
DB 181 SOKLPTMLAEMTSPVIVKRNASTYSGTGVKRNRYGSDOCLRLDVPVPPSNRAGTIA 240
QY 241 GAVIGVTLALVIGLIIFFCCR 261
DB 241 GAVIGVTLALVIGLIIFFCCR 261

RESULT 6
US-09-990-444-505

Sequence 505, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1c19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033

PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23

PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80;

Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCEVLLCGVADLTRSLSTTTPEOMIEKAGETAYLPCRFLLGPEDEGPIIDIEWLLS 60
DB 1 MALLLCEVLLCGVADLTRSLSTTTPEOMIEKAGETAYLPCRFLLGPEDEGPIIDIEWLLS 60
QY 61 PANOKKDYVITILYSGKTYDDYVODLKGKRVHFTSNLKGSDASINTNLQSLDIGYQC 120
DB 61 PANOKKDYVITILYSGKTYDDYVODLKGKRVHFTSNLKGSDASINTNLQSLDIGYQC 120
QY 121 KVKKAPGVNKKIQLTFLKPSGTRCVVDGSEETIGNDFLXKCEPKESGLPLTYEMOKLSN 180
DB 121 KVKKAPGVNKKIHLVVLVPSGARCTVVDGSEETIGSFKIKCEPKESGLPLQTEMOKLSN 180
QY 181 SOKLPTLMAEMTSVIVSNASTSEYSGTYSCTVKNRVGSDOCLLRLLVPPSNRAGTIA 240

DB 181 SOKMPTSLMAEMTSVIVSNASSEYSGTYSCTVKNRVGSDOCLLRLLVPPSNRAGLIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 7
US-10-053-107-10
Sequence 10, Application US/10053107
Publication No. US20020192752A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Auecin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
FILE REFERENCE: P3033R1C1
CURRENT APPLICATION NUMBER: US/10/053,107
PRIOR FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 60/099601
PRIOR FILING DATE: 19998-09-09
PRIOR APPLICATION NUMBER: 60/107783
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 60/108802
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/218517
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: PCT/US99/00106
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 14

SEQ ID NO 10
LENGTH: 352
TYPE: PRT
ORGANISM: Homo Sapien
US-10-053-107-10

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLFEVLLCGVADLTRSITTPROMTEKAGETAYLCRFTLIGPEDEGPIIDIMLS 60
DB 1 MALLLFEVLLCGVADTPARSITTPBEMTEKAGETAYLCRFTLIGPEDEGPIIDIMLS 60
QY 61 PADNQRVDQYIILYSGDKIYDDYYODLKGHVHTSNDLKSAGSINVTNLQSLDIGTYQC 120
DB 61 PADNQRVDQYIILYSGDKIYDDYYODLKGHVHTSNDLKSAGSINVTNLQSLDIGTYQC 120
QY 121 KVKKAGVGNKKIQLTVLTKPSGTRCYVDGSEIINDFKLKEPKKESLPLEYWOKLSN 180
DB 121 KVKKAGVGNKKIQLTVLTKPSGTRCYVDGSEIINDFKLKEPKKESLPLEYWOKLSN 180
QY 181 SOKLPTLMLAEMTSPISVKNASTREYSGTSCVTKRVSGDQCLRLDVVPSPNRAGTIA 240
DB 181 SOKLPTLMLAEMTSPISVKNASTREYSGTSCVTKRVSGDQCLRLDVVPSPNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 8

US-09-989-730-505
Sequence 505, Application US/09989730
Publication No. US20020197674A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Nadjler, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989, 730
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
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PRIOR APPLICATION NUMBER: 60/088029
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PRIOR APPLICATION NUMBER: 60/088742
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PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
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PRIOR APPLICATION NUMBER: 60/088826
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PRIOR APPLICATION NUMBER: 60/088861
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PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
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PRIOR APPLICATION NUMBER: 60/089440
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PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532

1 PRIOR FILING DATE: 1998-06-17
2 PRIOR APPLICATION NUMBER: 60/089538
3 PRIOR FILING DATE: 1998-06-17
4 PRIOR APPLICATION NUMBER: 60/089598
5 PRIOR FILING DATE: 1998-06-17
6 PRIOR APPLICATION NUMBER: 60/089599
7 PRIOR FILING DATE: 1998-06-17
8 PRIOR APPLICATION NUMBER: 60/089600
9 PRIOR FILING DATE: 1998-06-17
10 PRIOR APPLICATION NUMBER: 60/089653
11 PRIOR FILING DATE: 1998-06-17
12 PRIOR APPLICATION NUMBER: 60/089801
13 PRIOR FILING DATE: 1998-06-18
14 PRIOR APPLICATION NUMBER: 60/089907
15 PRIOR FILING DATE: 1998-06-18
16 PRIOR APPLICATION NUMBER: 60/089908
17 PRIOR FILING DATE: 1998-06-18
18 PRIOR APPLICATION NUMBER: 60/089947
19 PRIOR FILING DATE: 1998-06-19
20 PRIOR APPLICATION NUMBER: 60/089948
21 PRIOR FILING DATE: 1998-06-19
22 PRIOR APPLICATION NUMBER: 60/089952
23 PRIOR FILING DATE: 1998-06-19
24 PRIOR APPLICATION NUMBER: 60/090246
25 PRIOR FILING DATE: 1998-06-22
26 PRIOR APPLICATION NUMBER: 60/090252
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29 PRIOR FILING DATE: 1998-06-22
30 PRIOR APPLICATION NUMBER: 60/090349
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32 PRIOR APPLICATION NUMBER: 60/090355
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34 PRIOR APPLICATION NUMBER: 60/090429
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38 PRIOR APPLICATION NUMBER: 60/090435
39 PRIOR FILING DATE: 1998-06-24
40 PRIOR APPLICATION NUMBER: 60/090444
41 PRIOR FILING DATE: 1998-06-24
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43 PRIOR FILING DATE: 1998-06-24
44 PRIOR APPLICATION NUMBER: 60/090472
45 PRIOR FILING DATE: 1998-06-24
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50 PRIOR APPLICATION NUMBER: 60/090542
51 PRIOR FILING DATE: 1998-06-24
52 PRIOR APPLICATION NUMBER: 60/090557
53 PRIOR FILING DATE: 1998-06-24
54 PRIOR APPLICATION NUMBER: 60/090676
55 PRIOR FILING DATE: 1998-06-25
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57 PRIOR FILING DATE: 1998-06-25
58 PRIOR APPLICATION NUMBER: 60/090690
59 PRIOR FILING DATE: 1998-06-25
60 PRIOR APPLICATION NUMBER: 60/090694
61 PRIOR FILING DATE: 1998-06-25
62 PRIOR APPLICATION NUMBER: 60/090695
63 PRIOR FILING DATE: 1998-06-25
64 PRIOR APPLICATION NUMBER: 60/090696
65 PRIOR FILING DATE: 1998-06-25
66 PRIOR APPLICATION NUMBER: 60/090862
67 PRIOR FILING DATE: 1998-06-26
68 PRIOR APPLICATION NUMBER: 60/090863
69 PRIOR FILING DATE: 1998-06-26
70 PRIOR APPLICATION NUMBER: 60/091360
71 PRIOR FILING DATE: 1998-07-01
72 PRIOR APPLICATION NUMBER: 60/091478
73 PRIOR FILING DATE: 1998-07-02

1 PRIOR APPLICATION NUMBER: 60/091544
2 PRIOR FILING DATE: 1998-07-01
3 PRIOR APPLICATION NUMBER: 60/091519
4 PRIOR FILING DATE: 1998-07-02
5 PRIOR APPLICATION NUMBER: 60/091626
6 PRIOR FILING DATE: 1998-07-02
7 PRIOR APPLICATION NUMBER: 60/091633
8 PRIOR FILING DATE: 1998-07-02
9 PRIOR APPLICATION NUMBER: 60/091978
10 PRIOR FILING DATE: 1998-07-07
11 PRIOR APPLICATION NUMBER: 60/091982
12 PRIOR FILING DATE: 1998-07-07
13 PRIOR APPLICATION NUMBER: 60/092182
14 PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2, 3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADTRSLSTTPPEQMIKAKGETAYLPCRFTLGPEDDGPIIDIEWLLS 60
1 MALLLCFVLLCGVADTRSLSTTPPEQMIKAKGETAYLPCRFTLSPEDDGPIIDIEWLLS 60
DB 1 PADMOKVDVILLYSGDKYDDYDYLKGRVHFTSNDLKSQDASINVTYLOJSDICTYQC 120
QY 61 PADMOKVDVILLYSGDKYDDYDYLKGRVHFTSNDLKSQDASINVTYLOJSDICTYQC 120
DB 61 PADMOKVDVILLYSGDKYDDYDYLKGRVHFTSNDLKSQDASINVTYLOJSDICTYQC 120
QY 121 KYKAPGVGNKKIQLVLLKPSGTRCYVDGSEIIGNDFLKEPKEGSLPLLYEWOXLSN 180
121 KYKAPGVANKIHLVLLKPSGARCIVDGESEIGDFIKKEPKEGSLPLQYEWOKLD 180
QY 181 SQKLPFLMLAEMTSPVIVSNASTEXSGTYSCTVKNRVSSDOCLRLDVPPSPNAGTIA 240
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QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 9
US-09-990-436-505
Sequence 505, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990, 436

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; PRIOR FILING DATE: 1998-07-09

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Query Match          91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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RESULT 10
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; Sequence 505, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guerne, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
; CURRENT FILING DATE: 2001-11-16
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;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred No. 2, 3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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RESULT 11
US-09-993-687-505
; Sequence 505, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
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; APPLICANT: Fong, Sherman
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; APPLICANT: Goddard, Audrey

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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLFEVLICGVADLTFRSLSTTPROMTEKAGETAYLPKRTTLGPEDOGPIDIMWLIS 60
DB 1 MALLFEVLICGVADLTFRSLSTTPROMTEKAGETAYLPKRTTLGPEDOGPIDIMWLIS 60
QY 61 PADNOKVDVYIIYSGDKIYDDYYODLKGHVFTSNDLKSQDASINVTNLQSLDIGTYOC 120
DB 61 PADNOKVDVYIIYSGDKIYDDYYODLKGHVFTSNDLKSQDASINVTNLQSLDIGTYOC 120
QY 121 KYKABGVGNKKIQLTVLLKPSGTRCYVDGSEIEIGNDFLKCPEKSGSLPLYEMOKLSN 180
DB 121 KYKABGVGNKKIQLTVLLKPSGTRCYVDGSEIEIGNDFLKCPEKSGSLPLYEMOKLSN 180
QY 181 SQKLPFLMLAEMTSPIYSVKNASTETSGTSCVAKRVSGDQCLRLDVPSPNRAGTTA 240
DB 181 SQKLPFLMLAEMTSPIYSVKNASTETSGTSCVAKRVSGDQCLRLDVPSPNRAGTTA 240
QY 241 GAVIGVLLALVLGLIIFCCR 261
DB 241 GAVIGVLLALVLGLIIFCCR 261

RESULT 12
US-09-899-734-505
; Sequence 505, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Geritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tuma, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P27301C64
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
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;; PRIOR FILING DATE: 1997-11-24
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;; PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Fred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLCFVLLCGVADLTRELSITTPPEOMTEKAKGETAYVPCRFITGPEPDQGLDIEMLS 60
DB 1 MALLCFVLLCGVADLTRELSITTPPEOMTEKAKGETAYVPCRFITGPEPDQGLDIEMLS 60
QY 61 PADNOKVDVILLYSGDKYIDYDYLKGRVHFTSNDLSKGDASINVTNLQSLDICTYOC 120
DB 61 PADNOKVDVILLYSGDKYIDYDYLKGRVHFTSNDLSKGDASINVTNLQSLDICTYOC 120
QY 121 KYKAPGVNKKIQLTVLLKPSGTRCVYNGSEIGNDFLKEPEKGSLLPLYEMOKLSN 180
DB 121 KYKAPGVNKKIHLVLLKPSGARCVYNGSEIGSDFIKCEPEKGSLLPLYEMOKLSN 180
QY 181 SOKLFTMLAEMTSPVSYKNASTEXSGTYSCTVKRNVGSDOCLRLDVPSPSNRAGTIA 240
DB 181 SOKMFTSWLAEMTSSVSYKNAASSEYSGTYSCTVRNVGSDOCLRLNVPPSNRAGTIA 240
QY 241 GAVIGVLLALVILGLIIFCCR 261

DB 241 GATIGTLALALGLIIFCCR 261

RESULT 13
US-09-997-653-505
Sequence 505, Application US/09997653
Publication No. US20030008297A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC3
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;

Best Local Similarity 89.3%; Pred. No. 2,36-80; Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLICVLLCGVADLTRSLITTPEDOMIEKAKETAYLPCRFLLGPDGGLDIEWLIS 60
DB 1 MALLICVLLCGVADLTRSLITTPEDOMIEKAKETAYLPCRFLLGPDGGLDIEWLIS 60
QY 61 PADNOKDOYIILYSSGKIYDDYQDLKGRVHTFNSDLKSGDASINTVNLQSLDIGTYOC 120
DB 61 PADNOKDOYIILYSSGKIYDDYQDLKGRVHTFNSDLKSGDASINTVNLQSLDIGTYOC 120
QY 121 KVKKAPGVANKKIOTLVLLKPSGTRCYVDGSEIEGNDPFLKCEPKESLPLLYEWOKLSN 180

DB 121 KVKKAPGVANKKIOTLVLLKPSGTRCYVDGSEIEGNDPFLKCEPKESLPLLYEWOKLSN 180
QY 181 SQKPLTLMLEMTSPVIVSKNASTEXSGTYSCTVKNRVSSDCLRLDVPVPSNRAGTIA 240
DB 181 SQKPLTLMLEMTSPVIVSKNASTEXSGTYSCTVKNRVSSDCLRLDVPVPSNRAGTIA 240
QY 241 GAVIGVLLALVILGLIIFCCR 261
DB 241 GAVIGVLLALVILGLIIFCCR 261

RESULT 14
US-09-993-667-505
Sequence 505, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C4
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2.3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 1998-07-09

Query Match      91.1%; Score 1238; DB 9; Length 352;
Best Local Similarity 89.3%; Pred. No. 2,3e-80;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0

QY      1 MALLLCFVLLCGVADLTRSLSTITPEQMIERAKGETAYLPCRFTLGPEDQGLDIEMLLS 60
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Db      1 MALLLCFVLLCGVADPARSLSTITPEEMIERAKGETAYLPCRFTLSPEDQGLDIEMLLS 60
        |||||

QY      61 PADNOKVDQVILLYSGDKIYDDYODLKGRAHTFSNDLKSGDASINVTNLQSLDICTYOC 120
        |||||
Db      61 PADNOKVDQVILLYSGDKIYDDYFDLKGRAHTFSNDLKSGDASINVTNLQSLDICTYOC 120
        |||||

QY      121 KVKKAPGVGNKKIQTLTVLKLPSGTRCYVDGSEIGNDPKLKEPREGSLPLIYEWOKSN 180
        |||||
Db      121 KVKKAPGVANKKIHLYVLVYKPSGARCYVDGSEIGSDPKIKEPREGSLPLIYEWOKSD 180
        |||||

QY      181 SQKPLTLLAEMTSVLSVKNASSTEGSYCTVKNRGSDQCLRLVDVPPSNRAGTIA 240
        |||||
Db      181 SQKPLTLLAEMTSVLSVKNASSTEGSYCTVKNRGSDQCLRLVNVPPSNRAGLIA 240
        |||||

QY      241 GAVIGVLLALVLIHLIFCCR 261
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Db      241 GAVIGTLLALVLIHLIFCCR 261
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Search completed: July 9, 2003, 12:46:45
Job time : 26 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2003, 12:43:23 ; Search time 18 Seconds
(without alignments)
1393.949 Million cell updates/sec

Title: US-09-899-634c-2

Perfect score: 1359

Sequence: 1 MALLLCFVLLCGVADLTRSL.....AVIGVLLAVLIGLIIFCCR 261

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1270 | 93.5 | 365 | 2 JC7780 | coxsaackie- and ade |
| 2 | 196 | 14.4 | 299 | 2 S56749 | junctional adhesio |
| 3 | 159.5 | 11.7 | 4162 | 2 T42633 | connectin/citin - |
| 4 | 159 | 11.7 | 5175 | 2 T20992 | hypothetical prote |
| 5 | 154 | 11.7 | 5198 | 2 T43290 | hemiscentin precurs |
| 6 | 154 | 11.3 | 309 | 2 I49503 | B-lymphocyte activ |
| 7 | 151 | 11.1 | 7962 | 2 I38346 | elastic titin - hu |
| 8 | 144 | 10.6 | 526 | 2 A37821 | butyrophilin - bov |
| 9 | 143 | 10.5 | 483 | 2 T17346 | hypothetical prote |
| 10 | 139.5 | 10.3 | 1091 | 2 A58532 | glial cell membran |
| 11 | 136.5 | 10.0 | 518 | 2 JC4024 | poliovirus recepto |
| 12 | 136.5 | 10.0 | 3707 | 2 S18252 | heparan sulfate pr |
| 13 | 131 | 9.6 | 1323 | 2 PNO568 | connectin 3B - chi |
| 14 | 129.5 | 9.5 | 4391 | 2 A38096 | perlecan precursor |
| 15 | 128 | 9.4 | 526 | 2 S70887 | butyrophilin precu |
| 16 | 127.5 | 9.4 | 344 | 2 I56551 | neurotrophin - rat |
| 17 | 127.5 | 9.4 | 464 | 2 C30127 | transmembrane carc |
| 18 | 127.5 | 9.3 | 526 | 1 A32164 | biliary glycoprote |
| 19 | 127 | 9.3 | 509 | 2 JC5288 | SHP substrate-1 pr |
| 20 | 127 | 9.3 | 513 | 2 JC5289 | SHP substrate-1 pr |
| 21 | 127 | 9.3 | 764 | 2 A49448 | irregular chlam C |
| 22 | 126 | 9.3 | 246 | 1 A32959 | myelin p0 protein |
| 23 | 124 | 9.1 | 1336 | 2 I60558 | Fil-1 tyrosine kin |
| 24 | 123.5 | 9.1 | 538 | 2 JC2457 | vascular cell adhe |
| 25 | 123.5 | 9.1 | 2222 | 2 T13924 | sck protein - frui |
| 26 | 122.5 | 9.0 | 647 | 2 B41288 | vascular cell adhe |
| 27 | 122.5 | 9.0 | 739 | 2 A41288 | vascular cell adhe |
| 28 | 122 | 9.0 | 584 | 2 T08678 | hypothetical prote |
| 29 | 121.5 | 8.9 | 738 | 2 A40096 | platelet-endotheli |

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| 30 | 121 | 8.9 | 247 | 2 A55717 | myelin/oligodendro |
| 31 | 120.5 | 8.9 | 523 | 2 I50478 | neurotin - goldfif |
| 32 | 120 | 8.8 | 811 | 2 A41054 | fasciclin II, tran |
| 33 | 120 | 8.8 | 873 | 2 B41054 | fasciclin II pi-1i |
| 34 | 119.5 | 8.8 | 392 | 1 RWHUPD | poliovirus recepto |
| 35 | 119.5 | 8.8 | 417 | 1 RWHUPA | poliovirus recepto |
| 36 | 119.5 | 8.8 | 1052 | 2 B49120 | protein-tyrosine k |
| 37 | 119 | 8.8 | 1896 | 2 T08851 | Down syndrome cell |
| 38 | 118.5 | 8.7 | 329 | 1 A48754 | B7-2 antigen - hum |
| 39 | 118.5 | 8.7 | 478 | 2 I53960 | PRR2 alpha - human |
| 40 | 118.5 | 8.7 | 1011 | 2 T13659 | neurotrophin - fr |
| 41 | 118 | 8.7 | 358 | 2 I68093 | PRR2 delta - human |
| 42 | 118 | 8.7 | 1033 | 2 S19247 | cell adhesion prot |
| 43 | 117.5 | 8.6 | 1176 | 2 JN0583 | myosin-light-chain |
| 44 | 116.5 | 8.6 | 333 | 2 A31923 | amalgam protein pr |
| 45 | 116.5 | 8.6 | 898 | 2 A40114 | fasciclin II precu |

ALIGNMENTS

RESULT 1

JC7780 coxsackie- and adenovirus receptor - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #ext_change 02-Apr-2002

C/Accession: JC7780

R/Thoeien, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.

Biochem. Biophys. Res. Commun. 288, 805-808, 2001

A/Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recept

A/Reference number: JC7780

A/Contents: Liver

A/Molecule type: mRNA

A/Residues: 1365 <THO>

A/Cross-references: GB:AY033651

C/Comment: This protein serves as the primary adenoviral attachment site on bovine cell

Query Match 93.5%; Score 1270; DB 2; Length 365;

Best Local Similarity 93.1%; Pred. No. 3e-90;

Matches 242; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

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| DB | 61 | PADNOKVDOYIIYSGDKIYDDYODLKGKRVHFTSNDLKSASINVTLQLSDIGTYQC | 120 |
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| QY | 181 | SGKLPTMLAEMTSPVIVSNASTESGYSTCVKRVGSDQCLRLDVVPSPNRACTIA | 240 |
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| DB | 241 | GAVIGVLLAVLIGLIIFCCR | 260 |

RESULT 2

S56749 junctional adhesion molecule precursor - human

N/Alternate names: Fli platelet antigen; platelet adhesion molecule PAM-1; platelet Fli

C/Species: Homo sapiens (man)

C/Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #ext_change 01-Feb-2002

C/Accession: A59406; S56749

R/Ozaki, H.; Ishii, K.; Hotiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.;

J. Immunol. 163, 553-557, 1999

A/Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut

R,Vogel, B.E.; Hedgescock, E.M.
 Submitted to the EMBL Data Library, June 1998
 A:Description: Hemiscutinin is required for hemidesmosome mediated cell adhesion and germ-
 A:Reference number: 222396
 A:Accession: T43290
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-5198 <VOG>
 A:Molecule type: mRNA
 A:Cross-references: EMBL:AF074901; PIDN:AA26792.1
 R:Stalstrom, J.
 Submitted to the EMBL Data Library, December 1994
 A:Reference number: 219355
 A:Accession: T20993
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <WIL>
 A:Cross-references: EMBL:Z47066; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F1569.4b
 A:Experimental source: clone F15G9
 R:Keshaw, J.
 Submitted to the EMBL Data Library, December 1994
 A:Reference number: 219929
 A:Accession: T24734
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5198 <W12>
 A:Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F1569.4b
 A:Experimental source: clone T09B9
 C:Genetics:
 A:Gene: him-4; F15G9.4b
 A:Map position: X
 A:Intons: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
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 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/

Query Match 11.7%; Score 159; DB 2; Length 5198;
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12 GVADLFRSLSTITPEQMI-----KAKGETAVLPKCFITGPDGQPLDIEMLLSPADNQ 65
 3845 GVELELVLDVFPFPPVSVSNDPIKALGETITLFCVAGSNPVPQ-----LKW----- 3892
 Db 66 KVDQVITLVSGDKIYD---YYODLKGRVHTSNDLKSQDASINVTNLQSLDICTGYCKV 122
 Qy 3893 -----AKGSLIFPSPDARISLKG-----ARIDIPHLKKTVDGDTYCCQ 3932
 Db 123 KKAPEGVNKKIQLTLVLKPEGTRCYVDGSEIENDFLKCPEKPGSLPLLYEMQKLSNQ 182
 Qy 3933 LNAAGTSEASVSVDVLPPEINRDIDMSPL-----PAQQSITL-----QCLAQCK 3979
 Db 183 KLPTL-WLAEMT-----SPVTSVKNASTREVSCTYKKNVSGSDQCLRL 227
 Qy 3980 PIVQMRKTLNGTALHTSTPGITVASDSTFIQINNVSLSKGVYTAENVAGSDNIMVYN 4039
 Db 228 DVV--PPSNRAGT---IAG--AVIGVL 248
 Qy 4040 DVVQAPVINSKGTQKQVIEGELAVIECV 4067

RESULT 6
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 B-Lymphocyte activation antigen 7 precursor - mouse
 N:Alternate names: MB7-2
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
 C:Accession: I49503; S17291; I49521
 R:Selvakumar, A.; White, P.C.; Dupont, B.
 Immunogenetics 38, 292-295, 1993
 A:Title: Genomic organization of the murine B-Lymphocyte activation antigen B7.
 A:Reference number: I49503; MUID:9330789; PMID:766531
 A:Accession: I49503
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-309 <RES>
 A:Cross-references: GB:I12589; NID:9293299; PIDN:AAA7240.1; PID:9293301
 R:Freeman, G.J.; Gray, G.S.; Gimm, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Fingero
 J. Exp. Med. 174, 625-631, 1991
 A:Title: Structure, expression, and T cell costimulatory activity of the murine homolo
 A:Reference number: S17291; MUID:91341422; PMID:1714935
 A:Accession: S17291
 A:Molecule type: mRNA
 A:Residues: 1-274; R', 279-309 <PRE>
 A:Cross-references: EMBL:X60958; NID:950111; PIDN:CAA43291.1; PID:950112
 R:Inobe, M.; Linley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Ueda, T.
 Biochem. Biophys. Res. Commun. 200, 443-449, 1994
 A:Title: Identification of an alternatively spliced form of the murine homologue of B7.
 A:Reference number: I49521; MUID:94220123; PMID:7513163
 A:Accession: I49521
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-143; 238-274; R', 279-309 <RE2>
 A:Cross-references: GB:D16220; NID:9505118; PIDN:BA03748.1; PID:9994769
 C:Genetics:
 A:Gene: B7
 A:Intons: 37/1; 143/1; 237/1; 275/1
 C:Superfamily: B-Lymphocyte restricted antigen B7
 C:Keywords: alternative splicing

Query Match 11.3%; Score 154; DB 2; Length 309;
 Best Local Similarity 22.9%; Pred. No. 0.00017;
 Matches 65; Conservative 55; Mismatches 108; Indels 56; Gaps 13;

3 LLLCFVLLCGVADLFRSLSTITPEQMIERAKGETAVLPKCFITGPDGQPLDIEMLLSPA 62
 Db 21 LILLFVLLIRLSQVSSDV-----DEQLSKSVKDKVLLPCRVNSPHDESDRIYW----- 70
 Qy 63 DNQKNDQVIT-LYSGP-KIYDDYODLKGRVHTSNDLKSQDASINVTNLQSLDICTGYCC 120
 Db 71 --QKHKKVAVSLVAGLKWPEY---KRRITLYDNTY---SLIILGLVLSDRGYSC 119
 Qy 121 KYKAPGVNKKIQLTLVLKPS-----GTRCYVDGSEIENDFLKCPEKPGSLPLLYEM 175
 Db 120 VVQKKER-GTYEVKHALVALKLSIKADFTSPNITESGNPDAOTKRTICFASGEPKRFWS 178
 Qy 176 QKLSNQKLPITLWLAEMTSPVTSVKNAST-EYSGTGCTYKKNVSGSDQCLRL----- 227
 Db 179 --LENGRELPGINTTISQPESELTYTSSQLDENTTRNHTIK-----CLIKYGDAHVS 229
 Qy 228 -----DVVPPSNRAGTIGAVIGVLLAVLIGLIFC-CR 261
 Db 230 EDFTEKPEPDPDSKNTLVLFAGAGAVITVIVIVIIKCFCK 273

RESULT 7
 I38346
 elastic titin - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: I38346
 R:Labat S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A:Reference number: A57430; MUID:96026330; PMID:7569978
 A:Accession: I38346
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-7962 <RES>
 A:Cross-references: EMBL:X90569; NID:91017426; PIDN:CAA62189.1; PID:91017427
 C:Genetics:
 A:Gene: GDB:TTN
 A:Cross-references: GDB:127867; OMIM:188840
 A:Map position: 2q31-2q31

Query Match 11.1%; Score 151; DB 2; Length 7962;
 Best Local Similarity 23.9%; Pred. No. 0.015;
 Matches 61; Conservative 31; Mismatches 77; Indels 86; Gaps 12;

| | | | |
|----|------|---|------|
| QY | 12 | GVAIDTRLSLTTP-----BOMIEKAGEATVLECFRTLPBPDG--PLDIEMILSPAD | 63 |
| Db | 4050 | GSASSSTSLKXKEPRPIFRKKHPRIETLKGADVHLEC-----ELQGTPRHVS----- | 4097 |
| QY | 64 | NQKVDVQVILLSGDKIYDYQDLKGRVHTSNLKSQD-----ASINVTNLQLS | 113 |
| Db | 4098 | -----YKD-----KRELRSGKKYKXIMSENFELTIIHILNDVAA | 4129 |
| QY | 114 | DIGTYOCKVKKAPGAVGNKKIQULYVLK--PSGTRCVYVGSEIGNDFLTKCEPKRGSJPL | 171 |
| Db | 4130 | DIGERYQCKATN--DVGSDTCVGSIALKKPPRPVKLSIISTIVGKEVLO--TTIEGAPPI | 4186 |
| QY | 172 | LYEMOK-----LSNSOKLPTLMLAEMTSPVISYKNASTEYSGTYSCTVKNRV | 218 |
| Db | 4187 | SVVVFKEKGELIVREEDNIMISYSENIALTQFSR-----VEPANA-----GRYTCQIKNDA | 4236 |
| QY | 219 | GSDOCLRLDVPVPS | 233 |
| Db | 4237 | GMQECFATLSVLEPA | 4251 |

RESULT 8
A37821
butyrophilin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-Nov-1999
C:Accession: A37821
R:Jack, L.J.W.; Mather, I.H.
J. Biol. Chem. 265, 14481-14486, 1990
A:Title: Cloning and analysis of cDNA encoding bovine butyrophilin, an apical glycoprotein
A:Reference number: A37821; MUID:90354441; PMID:2387867
A:Accession: A37821
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-526 <JAC>
A:Cross-references: GB:M5551; MID:g1763685; PIDN:AAB39766.1; PID:g162773
C:Keywords: transmembrane protein

| | | | | |
|-----------------------|-------|------------------|--------|----------------|
| Query Match | 10.6% | Score 144 | DB 2 | Length 526 |
| Best Local Similarity | 23.4% | Pred. No. 0.0019 | | |
| Matches | 67 | Conservative | 50 | Mismatches 113 |
| | | | Indels | 56 |
| | | | Gaps | 13 |

| | | | | |
|----|-----|---|-----|-----|
| QY | 4 | LICPLLCGVADLTSLSTITPEQMIIEAKGETAYLPCRFITGPDQGLDIEML--- | LS | 60 |
| | | : : | : : | : : |
| Db | 13 | LILFILFIDLPKLDASAPFDVIGQEDILIAVVGSDALPCRLSPNSAKG-MELIRMRERKYS | | 71 |
| | | : : | : : | : : |
| QY | 61 | PADNOKVDQVILILYSGDKIYDDYODLKGKRVHFTNDKSGDASINYNLQSDIGTYQC | | 120 |
| | | : : | : : | : : |
| Db | 72 | PA-----VYPSRSGQGESEEMAEHNGRVSIVSDHIAESGVAVRIQEVASDDGEVRC | | 124 |
| | | : : | : : | : : |
| QY | 121 | KVKKAPGVGNKKIQTLTVLILKPSGTRCYDGSSEIANDPKLK-----EPK----- | | 167 |
| | | : : | : : | : : |
| Db | 125 | FFRODENYEALIVHLKV--AALGSPHISMVKQESGEIQLEBTSVGWVPEEDVQMRTHRG | | 182 |
| | | : : | : : | : : |
| QY | 168 | SUPLILEWOKLSQSKLPTLWLAEMTSFVI-----SVKASTSEYGSCTVKN-RVGSQD | | 222 |
| | | : : | : : | : : |
| Db | 183 | E-----EPPSMSESNPDDEGLFTVRASVILIRDSMKV-----SCCIRNILLQGEK | | 229 |
| | | : : | : : | : : |
| QY | 223 | CLLRADV---VP-----PSNRAGTINGANIYGVLLALVILIGLIIFCCR | | 261 |
| | | : : | : : | : : |
| Db | 230 | -----DVEVSIIPASEFPFRLTPMWWAAVAILLVLLGLLTGGSIFFTFR | | 270 |
| | | : : | : : | : : |

RESULT 9
T17346
hypothetical protein DKFZ58601624.1 - human (Fragment)
C|Species: Homo sapiens (man)
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 15-Oct-1999
C|Accession: T17346
R|Dussterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999

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A:Reference number: Z18727
A:Accession: T17346
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-483 <DUS>
A:Cross-references: EMBL:AL117666
A:Experimental source: adult uterus; clone DKFZp58601624
C:Genetics:
A>Note: DKFZp58601624.1

Query Match      10.5%  Score 143;  DB 2;  Length 483;
Best local Similarity 26.3%;  Pred. No. 0.0021;
Matches 41;  Conservative 31;  Mismatches 80;  Indels 4;  Gaps 3

```

QY 107 VTNLQSDISTGTQCKKAPGVGNKKIKQIVYLKSGRGCVDSSEIANDPFKCKBPKE 166
 Db 49 ITPVKIDDDAGVNSTQNSAGSISANNATLVLETPSLVLPEDRVDVSGETVALQCK-AT 10707
 QY 167 GSPLLYEOKLSNSOKLPTLWLAEMTSFVSIYKNASTREYSGTSCYKQNVGSDQCLIR 222
 Db 108 GNPFRPIYTFKQDRPLSTLRHNHLPRNQDLVQNVVAEDAGRTCEMSNTLGERAHSQ 167
 QY 227 LDVVPSP--NRAGTNGA-VIGVLADVLIGLIFC 259
 Db 168 LSVLPAGCKRQDLTVGIFTIAVVSIVLTSLWVC 203

RESULT 10
A58532
glial cell membrane glycoprotein LIG-1 precursor - mouse
C1Species: Mus musculus (house mouse)
C1Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
C1Accession: A58532
R1Sturuk1, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
J. Biol. Chem. 271, 22522-22527, 1996
A1Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in
A1Reference number: A58532; MUID:96394313, PMID:8798419
A1Accession: A58532
A1Status: preliminary; translated from GB/EMBL/DBD

A.Residues: 1-1091 <SVZ>
A.Cross-references: GB:D87572; NID:g1545806; PDB:5AA11416.1; PID:g1545807
C.Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan amino-te
F.356-61/Domain: proteoglycan alpha-terminal homology <PAH>
F.71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F.793-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F.118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F.142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F.166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F.191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F.214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F.238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F.262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F.286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F.310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F.334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F.358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F.385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F.409-433/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F.440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>

| | | | | | | | |
|-----------------------|-------|--------------|----------|------------|-----|--------|------|
| Query Match | 10.3% | Score | 139.5 | DB | 2 | Length | 1091 |
| Best Local Similarity | 24.0% | Pred. | No. 0.01 | | | | |
| Matches | 55 | Conservative | 37 | Mismatches | 106 | Indels | 31 |
| | | | | | | Gaps | 9 |

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Oy      34  GEAIVALEPCRTLPPEOGGLDIEMWLSPADNOKVQVILVSGDIYDDYVODLKSGVNF  93
Db      615  GTTARLECAATGHPNQ-----IAW-----QK-----DGG-----TDFARERAMHV  655
Oy      94  TSNDLKSGDASIVNTNLQSDIGTQYCKKKAPGVGNKKIQLTYLKRSGIRCYVDSSE  155
Db      653  MPDQ---DVFF-IITVKKIDMGVYSCTAQNDSAGVSANATITVLETSTSLAVPLEDRV  707

```

QY 154 IGDPLKIKCPKSGSLPLYEWOKLSQCLPTLWLAEMTSPVISVKNASTEYSGTYSCT 213
 Db 708 VGETVAFOCKVATSPPTPRI-TWLKGRPLSLTERHHFTPNQMLLVQNVIMIDAGRYTCE 766
 QY 214 VKRNVSDQCLLDVVP--SNRAGTIAGA-VIGVLLAVLGLIIFC 259
 Db 767 MSNPLGTERASHQSILPTPGCKRKDGTTVGIFTIIVACISVLISLWVC 815

RESULT 11

JC4024
 poliovirus receptor-related protein precursor - human

C/Species: Homo sapiens (man)

C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999

C/Accession: JC4024

R/Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubz

Gene 155, 261-265, 1995

A/Title: Complementary DNA characterization and chromosomal localization of a human gene

A/Reference number: JC4024; MUID:95237621; PMID:7721102

A/Accession: JC4024

A/Molecule type: mRNA

A/Residues: 1-518 <LOP>

A/Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796

C/Genetics:

A/Gene: GDB:PVRR1

A/Cross-references: GDB:583951

A/Map position: 11q23-11q24

C/Superfamily: poliovirus receptor; immunoglobulin homology

C/Keywords: glycoprotein; transmembrane protein

F/1-30/Domain: signal sequence #status predicted <SIG>

F/31-518/Product: poliovirus receptor-related protein #status predicted <MAT>

F/356-379/Domain: transmembrane #status predicted <TM>

F/36,72,82,139,287,308,333/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 10.0%; Score 136.5; DB 2; Length 518;

Best Local Similarity 18.5%; Pred. No. 0.0072;

Matches 67; Conservative 50; Mismatches 86; Indels 159; Gaps 17;

QY 34 GETAVLPICRFTLPEDQGLDIEMLSPADNOKVDV-----ILYS--GDK 78

Db 44 GTDVVLHCSFA-----NPLPSVKITQVTWOKSTNGSKONVAITNPSMGVS 88

QY 79 IYDDYQDLKGRVHTFSNDKSGDASINVTNLSIDIGYQCKVKAPGVGNKKIQ--LT 136

Db 89 VLAPY-----RERVFLRPST--DGTIRSLLEDEGVIYCEPATRP--TGNRESQNLRT 141

QY 137 VLLKPSGTRCYVNGSEI-----GNPKL--KCEPEGSLPLYEWQ-KLSNSQKLP-- 185

Db 142 VMKAPTN--WIGTQAVLRAKKGQDDKVLVATCTSANGRPVSVMETLKGEARVPGD 198

QY 186 -----TWLAEMTSPVISVKN----- 201

Db 199 SGTPMAVTVISRYRLVPSREAHQSLACIVNTHMDFKESLTILNVOYEVEVTIEGDGN 258

QY 202 -----ASTEY-----SGTYSCT 213

Db 259 WYLQRMVDVLTCKADANRPATEYHMTTLNGLPKGVEAQNRTLPFKSPIYSLAGTYICE 318

QY 214 VKRNVSDQCLLDV-----PSN--RAGTIAGAVG-----VLALVLLGLIIFC 259

Db 319 ATNPITGRSGVEVNITEPPTSPPEHGRAGVPFAIIGVAGSILVLIIVGGIIVA 378

QY 260 CR 261

Db 379 LR 380

RESULT 12

S18252
 heparan sulfate proteoglycan - mouse

N/Alternate names: perlecan

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C/Accession: S18252; A31917; B31917; S66460
 R/Noonan, D.M.; Fulle, A.; Valente, P.; Cal, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; H
 J. Biol. Chem. 266, 22939-22947, 1991

A/Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteog
 adhesion molecule.

A/Reference number: S18252; MUID:92078153; PMID:1744087

A/Accession: S18252

A/Molecule type: mRNA

A/Residues: 1-3707 <NOO>

A/Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296

R/Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogel, G.; Sasaki, M.; Yamada, Y.; Has

J. Biol. Chem. 263, 16379-16387, 1988

A/Title: Identification of cDNA clones encoding different domains of the basement membr-

A/Reference number: A92680; MUID:89034110; PMID:2972708

A/Accession: A31917

A/Molecule type: mRNA

A/Residues: 940-1601 <NO2>

A/Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253

A/Accession: B31917

A/Molecule type: mRNA

A/Residues: 1870-2600 <NO3>

A/Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301

R/Schulze, B.; Mann, K.; Böttcher, R.; Wiedemann, H.; Timpl, R.

Eur. J. Biochem. 231, 551-556, 1995

A/Title: Structural properties of recombinant domain IIR-3 of perlecan containing a gloi

A/Reference number: S66460; MUID:95377282; PMID:7649154

A/Accession: S66460

A/Molecule type: protein

A/Residues: 1272-1274, 'X', 1276, 'X', 1278-1279 <SCH>

C/Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G rep-

C/Keywords: glycoprotein

F/199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F/285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F/325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F/368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F/764-811/Domain: laminin-type EGF-like homology <LEG3>

F/1159-1206/Domain: laminin-type EGF-like homology <LEG7>

F/1563-1610/Domain: laminin-type EGF-like homology <EG7>

F/1613-1668/Domain: laminin-type EGF-like homology <LEG8>

F/3163-3198/Domain: EGF homology <EGF>

F/3270-3423/Domain: laminin G repeat homology <LEG>

F/3464-3482/Domain: EGF homology <EGF7>

F/1256,1891,2336,2394,2427/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 10.0%; Score 136.5; DB 2; Length 3707;

Best Local Similarity 21.3%; Pred. No. 0.079;

Matches 61; Conservative 38; Mismatches 102; Indels 85; Gaps 12;

QY 20 LSTTPQWIEKAGETAVLPICRFTLPEDQGLDIEMLSPADNOKVDVITLYSGDKI 79

Db 2346 ISIEPPSSIVQ--QGDDAFKC--LIHGGAMPKIVEMKI--RDQLEENVHISPPGSI 2398

QY 80 -----YDDY--QDL-----KGRVH-----FTSNDLK 99

Db 2399 TIAPGPATMEPTACVANSVYAGQGVNLSVHGPTVSVLDEGPHVVMKXDTIECIS 2458

QY 100 SGD-----ASINVTNLSIDIGYQCKVKAPGVGNKK 132

Db 2459 SCEPRSPRWTRLGIVPKLEPRMFGIMSHAMIKLASVPSDAGTYVCAQNLGTAQIQ 2518

QY 133 IQLTV--LLKPSGTRCYVNGSE--EIGNDFLKCEPEGSLPLYEWOKLSNSQKLP 186

Db 2519 VELIVDTGTVAGOTPGVQVEBSLTLAEAGHTATLHGS-ATGNPPRIHMSK-----RAPI 2573

QY 187 LWLAEMTSPVISVKNASTEYSGTYSCTVKNVSGDCLLDVVP 232

Db 2574 PMQHRIGNTLVIPRAVQODSGOYICNATNSAGHTAATVVLHVESP 2619

RESULT 13

PN0568
 connectin 3B - chicken (fragment)

N/Alternate names: Cn3B protein

C:\Species: Gallus gallus (chicken)
C:\Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999
A:\Accession: P05068
R:\Matuyama, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanazawa, N.; Nakauchi, Y.; Kimura, S.
Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993
A:\Title: A novel domain sequence of connectin localized at the I band of skeletal muscle
A:\Reference number: P05068; MUID:9335602; PMID:8352787
A:\Accession: P05068
A:\Molecule type: mRNA
A:\Residues: 1-1323 <MAR>
A:\Cross-references: DDBJ:D16541, NID:g391629; PID:d1004495; PID:g391630
A:\Experimental source: Skeletal muscle
C:\Comment: This protein string-like single molecule spans from the Z line to the M line

Query Match 9.6%; Score 131; DB 2; Length 1323;
Best Local Similarity 23.7%; Pred. No. 0.06;
Matches 53; Conservative 31; Mismatches 90; Indels 50; Gaps 10;

OY 24 TPBQWIEKAKETATLPFRFTLGPDPGLDIEWILSPANDNQXVDQVITIIYSGRKITDDY 83
 |||:::||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 184 TPLEBVQVTVDSDASLQCVAGTPE---MTVSW-----YKGD----- 217
OY 84 YQDLKG----RVHFTSNLDKSGDASINVTNQLSDIGTYOCVKKAPGVGNKTQLTV-- 137
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 218 -TKLRGRTATVGMHF-----KNQVATLVESQVDSDDSGYICKVENTGCAIASSLLTYOE 271
OY 138 -LKPSGTCTCYVDSSEIIGNDFKLCKEPEKESGLPLYEWOK---LSNSQKLFPLMLAEW 192
 |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 272 RKLPPSPFRLKRLDVHEATVETGLPVTEPDC-GIASEPFEIVSWFDNDNVRYEDVYHTSFTDNV 330
OY 193 TSPVISVKNASTVEYSGTYSCTVKNRVG---SDQCRLRLDVPVP 232
 ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 331 A-ILOILIKTKSLIMGQYTCTASNAIGTASSSGKVLITEGKTP 372

RESULT 14
A38096

perlecan precursor - human
N:\Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate proteoglycan
C:\Species: Homo sapiens (man)
C:\Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text change 05-Nov-1999
A:\Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
R:\Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Tozzo, R.V.
J. Biol. Chem. 267, 8544-8551, 1992
A:\Title: Primary structure of the human heparan sulfate proteoglycan from basement membrane, laminin, neural cell adhesion molecules, and epidermal growth factor.
A:\Reference number: A38096; MUID:92235084; PMID:1569102
A:\Accession: A38096
A:\Molecule type: mRNA
A:\Residues: 1-4391 <MUR>
A:\Cross-references: GB:M65289; NID:G184426; PID:NAA52700.1; PID:G184427
R:\Kallunki, P.; Trygvason, K.
J. Cell Biol. 116, 559-571, 1992
A:\Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein with adhesive molecules, and epidermal growth factor.
A:\Adhesion number: A41736; MUID:92112994; PMID:1170768
A:\Accession: S19256
A:\Molecule type: mRNA
A:\Residues: 1-57; 'D', 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R', 91-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-4470
A:\Cross-references: EMBL:X62515; NID:g29469; PID:CMA44373.1; PID:g29470
R:\Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Trygvason, K.
Genomics 11, 389-396, 1991
A:\Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the gene
A:\Reference number: A41059; MUID:92120660; PMID:1685141

A:Accession: A41059
 A:Molecule type: mRNA
 A:Residues: 'R', 892-908, 'R', 910-1101, 'L', 1103-1132, 'L', 1134-1221, 'L', 1223-1397 <KA2>
 A:Cross-references: GB:S76436; NID:g243370; PIDN:AA21121.1; PID:g243371
 R:Dogge, G.R.; Kovalsky, I.; Chu, M.L.; Hassell, J.R.; McBride, G.W.; Yi, H.F.; Iozzo, Genomics 10, 673-680, 1991
 A>Title: Heparan sulfate proteoglycan of human gonads: partial molecular cloning, cellular
 A:Reference number: A40306; MUID:91365376; PMID:1679749
 A:Accession: A40306
 A:Molecule type: mRNA
 A:Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 <DOD>
 A:Cross-references: GB:M4283; NID:g184424; PIDN:AA52699.1; PID:g184425
 R:Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van de
 U:Cell Biol. 109, 3199-3211, 1989
 A>Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal
 A:Reference number: A33625; MUID:90078352; PMID:2687294
 A:Accession: B33625
 A:Molecule type: protein
 A:Residues: 1379-1384, 'X', 1386-1388, 'X', 1390-1398 <HE2>
 A:Accession: A33625
 A:Molecule type: protein
 A:Residues: 2166-2171, 'X', 2173-2175, 'X', 2177-2185 <HE3>
 A:Note: peptide potentially matches four different regions of sequence shown
 C:Genetics
 A:Gene: GDB:HSRPG2
 A:Cross-references: GDB:126372; OMIM:142461
 A:Map position: 1p36.1-1p36.1
 C:Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G rep
 C:Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembr
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:122-4391/Product: perlecan #status predicted <MAT>
 F:122-193/Domain: I <DOM1>
 F:194-530/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:199-234/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:285-319/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F:325-359/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:531-1676/Domain: I1 <DOM3>
 F:1159-1206/Domain: laminin-type EGF-like homology <LEG>
 F:1553-1610/Domain: laminin-type EGF-like homology <EGT>
 F:1613-1668/Domain: laminin-type EGF-like homology <LEG8>
 F:1677-3686/Domain: IV <DOM4>
 F:2007-2034/Domain: transmembrane #status predicted <TM>
 F:3687-4391/Domain: V <DOM5>
 F:3845-3880/Domain: EGF homology <EGF1>
 F:3888-3921/Domain: EGF homology <EGF>
 F:3953-4106/Domain: laminin G repeat homology <LG2>
 F:4177-4175/Domain: EGF homology <EGF2>
 F:4149-4151/Region: motor neuron attachment (L-R-E) motif
 F:4299-4301/Region: motor neuron attachment (L-R-E) motif
 F:65, 71, 76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
 F:89, 554, 1755, 2121, 3072, 3105, 3279, 3780, 3836, 4068/Binding site: carbohydrate (Aen) (cova
 F:2995, 3933, 4119/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

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DR EMBL; Y07593; CAA68868.1; --
DR EMBL; U90716; AAC51234.1; --
DR EMBL; AF169366; AAF05908.1; --
DR EMBL; AF169366; AAF05908.1; JOINED.
DR EMBL; AF169360; AAF05908.1; JOINED.
DR EMBL; AF169361; AAF05908.1; JOINED.
DR EMBL; AF169362; AAF05908.1; JOINED.
DR EMBL; AF169363; AAF05908.1; JOINED.
DR EMBL; AF169364; AAF05908.1; JOINED.
DR EMBL; AF169365; AAF05908.1; JOINED.
DR EMBL; AF200465; AAF24344.1; --
DR EMBL; HGNC:2559; CXADR.
DR MIM; 602621; --
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003600; IG_like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00408; IGG2; 1.
DR Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT TRANSMEM 238 258
FT DOMAIN 259 365
FT DOMAIN 34 127
FT DOMAIN 155 219
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FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;

Query Match 91.1%; Score 1238; DB 1; Length 365;
Best Local Similarity 89.3%; Pred. No. 5.7e-96;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLGCGVADLTRSLITTPQEMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLGCGVDFARSISITTPQEMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNQNQVDQVILLYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120
DB 61 PADNQNQVDQVILLYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120
QY 121 KVKAPGVGNKQIOLTVLLKPSGTRCYVDGSEIGNDFKLCRPPKESGLPLLYEWOKLSN 180
DB 121 KVKAPGVANKIHLVVLKPSGARCVCYVDGSEIGSDFKIKCEPKESGLPLQYEWOKLSD 180
QY 181 SOKLPTLWLAEMTSPLVSVKNASTSEYSGTYSCTVKNRVGSDOCLLRDLVVPPSNRAGTIA 240
DB 181 SQKMTPLWLAEMTSPLVSVKNASTSEYSGTYSCTVKNRVGSDOCLLRDLVVPPSNRAGLIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 2
CXAR MOUSE STANDARD; PRT; 365 AA.
AC P97752; O09052;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Coxsackievirus and adenovirus receptor homolog precursor (mCAR).
GN CXADR OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver;
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
RT "Isolation of a common receptor for Coxsackie B viruses and
RL adenoviruses 2 and 5.";
RN Science 275:1320-1323(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/MAI;
RX MEDLINE=97250541; PubMed=9096397;
RA Tomko R.P., Xu R., Philipson L.;
RT "HCAR and mCAR: the human and mouse cellular receptors for subgroup C
RT adenoviruses and group B coxsackieviruses.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;
RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B
RT viruses and adenoviruses.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y10320; CAA71368.1; --
DR EMBL; U90715; AAC53148.1; --
DR EMBL; Y11929; CAA72679.1; --
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003600; IG_like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00408; IGG2; 1.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat.
FT SIGNAL 1 19
FT CHAIN 20 365
FT DOMAIN 20 237
FT TRANSMEM 238 258
FT DOMAIN 259 365
FT DOMAIN 34 127
FT DOMAIN 155 219
FT DISULFID 41 120
FT DISULFID 162 212
FT CARBOHYD 106 106
FT CARBOHYD 201 201
FT CONFLICT 340 365
SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 89.5%; Score 1216; DB 1; Length 365;
Best Local Similarity 88.1%; Pred. No. 3.9e-94;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLGCGVADLTRSLITTPQEMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLGCGIADFTSGISITTPQREKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNQNQVDQVILLYSGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQC 120
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Qy 59 LSPADNQKVDVVIILYSGDKIKYDDYQDLKGRVHFTSNDLKSQDASINVTNQLSDIGTY 11
Db 64 FDQGDITFR---LVCYN-NKITASY-----EDRVTF-----LPTGITFKSVTR---EDTGY 107
Qy 119 QCKVKKAPG--VGNKKIQLTVLLAKPSGTRCVVDGSEEGINDPKLKCEPKESGLPILLYEQW 176
Db 108 TCMVSEGGNSYGEVKVKLIIVLPPSKFTVNI PSSATIGNRAVLTCSEODGSPPEYTFW 167
Qy 177 K-----LNSQKQLPTLMLAEMTSPVISVKRNASTEYSGTYSCTYKKNRVGSDQ 222
Db 168 KDGIVMTPNPKSTRAFSNSSVYVLTPTGTELVPDPLSASD-----TGEYSCEARNGVGTGM 222
Qy 223 C--LLRLDVVPPSNAGTTIAGAVGTGLLALVLGLIIF 258
Db 223 TSNVRAEAV--ERNVGVIVAA--VLVTLILGLILVF 255

RESULT 5
JAM2 HUMAN
ID ID JAM2 HUMAN STANDARD; PRT; 298 AA.
AC P57087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE JUNCTIONAL adhesion molecule 2 precursor (Vascular endothelial
DE JUNCTION-associated molecule) (VE-JAM).
GN JAM2 OR VEJAM OR C21ORF43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular endothelial cells;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
RA "Vascular endothelial junction-associated molecule, a novel member of
RA the immunoglobulin superfamily, is localized to intercellular
RA boundaries of endothelial cells.";
RT J. Biol. Chem. 275:19139-19145(2000).
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20507930; PubMed=10945976;
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjerkce R.J.,
RA Vanderhelme P., Morris A.P., Brock T.A.;
RA "A novel protein with homology to the junctional adhesion molecule:
RA Characterization of leukocyte interactions.";
RT J. Biol. Chem. 275:34750-34756(2000).
RL [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC SECONDARY LYMPHOID ORGANS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- DATABASE: NAME=PROW; NOTES=PROW 2.1-3 (2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186.g.htm".
CC
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DE Junctional adhesion molecule 1 precursor (JAM).
GN JAM1 OR JCAM1 OR JCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98327120; PubMed=9660867;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simmons D., Dejana E.;
RT "Junctional adhesion molecule, a novel member of the immunoglobulin
RT superfamily that distributes at intercellular junctions and modulates
RT monocyte transmigration.";
RL J. Cell Biol. 142:117-127(1998).
CC -!- FUNCTION: PLAYS A ROLE IN REGULATING MONOCYTE TRANSMIGRATION
CC INVOLVED IN INTEGRITY OF EPITHELIAL BARRIER. INVOLVED IN PLATELET
CC ACTIVATION.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: LOCALIZED AT TIGHT JUNCTIONS OF BOTH
CC EPITHELIAL AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U89915; AAC32982.1; --
CC MGD; MGI:1321398; Jcaml.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003600; Ig like.
CC Pfam; PF00047; Ig_2.
CC SMART; SM00410; Ig_like; 1.
CC SMART; SM00406; IG; 1.
CC KW Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal.
CC SIGNAL 1 26 POTENTIAL.
CC CHAIN 27 300 JUNCTIONAL ADHESION MOLECULE 1.
CC DOMAIN 27 238 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 239 259 POTENTIAL.
CC FT DOMAIN 260 299 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 42 115 IG-LIKE V-TYPE DOMAIN 1.
CC FT DOMAIN 145 219 IG-LIKE V-TYPE DOMAIN 2.
CC FT DISULFID 49 108 POTENTIAL.
CC FT DISULFID 152 212 POTENTIAL.
CC FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 300 AA; 32368 MW; 391F3E48FF3B97EC CRC64;
Query Match 11.98; Score 161.5; DB 1; Length 300;
Best Local Similarity 25.58; Pred. No. 2.5e-06;
Matches 65; Conservative 37; Mismatches 108; Indels 45; Gaps 11;
Qy 21 SITPQMIKAKGETAYLPCRTF--LGPEDQGPLDIEWLLSPADNOKVDQVILYSGDK 78
Db 29 SVYTAQSDVQVPENESIKLCTVSGFSSPR-----VEWKFV-----QGSTITALVCYN-SQ 77
Qy 79 IYDDYQDLKGRVHFTNDLKGDSINVTNLQLSDIGTYOCKYKAPG--VGNKKIQLT 136
Db 78 ITAPY-----ADRVTFSS-----SGITFSSVTRKNGEYTCMVSEGGQNYGEVSIHLT 126
Qy 137 VLLKPSGTRCVGDSSEIGNDFKLCKPKEGSLPLLWEWK-----LSNSQKLPTLWLA 190
Db 127 VLVPPSPKTTISPVSSVTIGNRAVLTCSEHGDSPSPSEYWFKDGISMLTADAKTRAFMNS 186
Qy 191 EMTSPVLSVKNASTEY-----SGTYSCTVKNRVGSDQCLRLDLVPPSPNRAGTIAGV 243

Db 187 SFT---IDPKSGDLIFDPVTFDPSGEYCYQAQNGYGT---AMRSEAAHMDAVELNVGGIV 240
Qy 244 IGVLLALVLIGLIIF 258
Db 241 AAVLVTLILGLLIF 255
RESULT 8
CD80_MOUSE STANDARD; PRT; 306 AA.
ID CD80_MOUSE
AC Q00609;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE antigen) (B7).
GN CD80 OR B7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=91341422; PubMed=1714935;
RA Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the
RT murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93307789; PubMed=7686531;
RA Selvakumar A., White P.C., Dupont B.;
RT "Genomic organization of the mouse B-lymphocyte activation antigen
RT B7.";
RL Immunogenetics 38:292-295(1993).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC MALIGNANCIES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
CC IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
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CC -----
CC EMBL: X60958; AAA43291.1; --
CC EMBL: L12589; AAA37240.1; ALT_SEQ.
CC EMBL: L12585; AAA37240.1; JOINED.
CC EMBL: L12586; AAA37240.1; JOINED.
CC EMBL: L12587; AAA37240.1; JOINED.
CC EMBL: L12588; AAA37240.1; JOINED.
CC PIR: S17291; S17291.
CC HSSP; P33681; LDR3.
CC MGD; MGI:101775; Cd80.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.

QY 121 KVKAPGVGNKKIQLTLLKSPGTRCYVDGSEBIGNDFKLK-----EPK-----EG 167
 Db 125 FFDENYEEAIVHLKV--AALGSDPHISMKVQESGEIQLECTSVGWYEPQVQWTHRG 182
 QY 168 SLPLLYEWQKLSNOKLPTLWLAEMTSPVI-----SVKNASTEYSGYCTVKNRVSQDQC 223
 Db 183 E-----EFPMSSESRNPDEGLFTVRASVIIRDSSMKV-----SCCIRNLLLGQEK 229
 QY 224 LRLDVPV---PSNRAGTIAGVIGVLLAIVLGLIFCCR 261
 Db 230 EVEVSPASFPFRLTPMVAIVLVLGLLTIGSIFFTWR 270

RESULT 10

PECL_PIG STANDARD; PRT; 740 AA.
 AC Q95242;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Platelet endothelial cell adhesion molecule precursor (PECAM-1)
 DE (CD31 antigen).
 GN PECAM1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nasu K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE EXPRESSED ON
 CC PLATELETS AND AT ENDOTHELIAL CELL INTERCELLULAR JUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 DR EMBL; X98505; CAA67129.1; -;
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00410; Ig_like; 1.
 KW Immunoglobulin domain; Glycoprotein; Cell adhesion; Transmembrane;
 KW Repeat; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 740
 FT BY SIMILARITY.
 FT PLATELET ENDOTHELIAL CELL ADHESION
 FT MOLECULE.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 28 602
 FT TRANSMEM 603 621
 FT DOMAIN 622 740
 FT DOMAIN 50 116
 FT DOMAIN 145 211
 FT DOMAIN 249 311
 FT DOMAIN 340 394
 FT DOMAIN 425 484
 FT DOMAIN 517 580
 FT DISULFID 57 109
 FT DISULFID 152 206
 FT DISULFID 256 304
 FT DISULFID 347 387
 FT DISULFID 432 477
 FT DISULFID 524 573
 FT CARBOHYD 52
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 357 357 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 436 436 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 740 AA; 82378 MW; F312DC62C4B4A217 CRC64;
 Query Match 10.0%; Score 136.5; DB 1; Length 740;
 Best Local Similarity 26.0%; Pred. No. 0.00094;
 Matches 47; Conservative 36; Mismatches 85; Indels 13; Gaps 6;

QY 84 YQDLKGRVHFTSNDLKSGDASINVNLQSLSDIGTYQC---KVKAPGVGNKKIQLTLLK 140
 Db 443 YQLKSGDLLASQNVSSNEPAVKDN-PTKDV-EYCIADNCHSHAGMPSKVRVKVIAP 500
 QY 141 PSGRICYVDGSEI--GNDFKLKCBPKGSLPLLYEWQKLSNOKLPTLWLAEMTSPVIS 198
 Db 501 VEEVKLSILLSEVESGQAIVLQCSVKESGSPITYKFYKEKENKPPHQVTLND-TQAIWH 559
 QY 199 VKNASTEYSGYCTVKNRVSQDCLRLDVPV-----PSNRAGTIAGVIGVLLAIVL 253
 Db 560 KPKASKDQEGQYCYCLASNRATPSKNFLOSNIILAVRVYLAPWKKGIAVVVIAVILL 619
 QY 254 G 254
 Db 620 G 620

RESULT 11

PGEM_MOUSE STANDARD; PRT; 3707 AA.
 ID PCBM_MOUSE
 AC Q05793;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Basement membrane-specific heparan sulfate proteoglycan core
 DE protein precursor (HSPG) (Perlecan) (PLC).
 GN HSPG2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Melanoma;
 RX MEDLINE=92078153; PubMed=1744087;
 RA Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M.,
 RA Yamada Y., Hassell J.R.;
 RT "The complete sequence of perlecan, a basement membrane heparan
 RT sulfate proteoglycan, reveals extensive similarity with laminin A
 RT chain, low density lipoprotein-receptor, and the neural cell adhesion
 RT molecule.";
 RL J. Biol. Chem. 266:22939-22947(1991).
 RN [2]
 RP SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=89034110; PubMed=2972708;
 RA Noonan D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M.,
 RA Yamada Y., Hassell J.R.;
 RT "Identification of cDNA clones encoding different domains of the
 RT basement membrane heparan sulfate proteoglycan.";
 RL J. Biol. Chem. 263:16379-16387(1988).
 CC -1- FUNCTION: This protein is an integral component of basement
 CC membranes. It is responsible for the fixed negative electrostatic
 CC charge and is involved in the charge-selective ultrafiltration
 CC properties. It serves as an attachment substrate for cells.
 CC -1- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
 CC dimers or stellate structures. It interacts with other basement
 CC membrane components such as laminin, prolargin and collagen type
 CC IV.

FT DISULFID 1594 1610 BY SIMILARITY.
 FT DISULFID 1613 1628 BY SIMILARITY.
 FT DISULFID 1615 1638 BY SIMILARITY.
 FT DISULFID 1641 1650 BY SIMILARITY.
 FT DISULFID 1653 1668 BY SIMILARITY.
 FT DISULFID 1792 1839 BY SIMILARITY.
 FT DISULFID 1886 1932 BY SIMILARITY.
 FT DISULFID 1976 2021 BY SIMILARITY.
 FT DISULFID 2073 2118 BY SIMILARITY.
 FT DISULFID 2170 2215 BY SIMILARITY.
 FT DISULFID 2268 2313 BY SIMILARITY.
 FT DISULFID 2365 2413 BY SIMILARITY.
 FT DISULFID 2456 2506 BY SIMILARITY.
 FT DISULFID 2554 2599 BY SIMILARITY.
 FT DISULFID 2641 2686 BY SIMILARITY.

Query Match 10.08; Score 136.5; DB 1; Length 3707;
 Best Local Similarity 21.3; Pred. No. 0.0069;
 Matches 61; Conservative 38; Mismatches 102; Indels 85; Gaps 12;

QY 20 LSITTPQMEKAGETAYLPCRTLGPDGGLDIEWLLSPADNQKVDVILYSGDKI 79
 2346 ISIEPSTVQ--QGQASPKC---LIHEGAMPIKVEWKI--RDQLEDNVHISPNGSII 2398
 80 -----YDDYY---QDL-----KGRVH-----FTSNDLK 99
 2399 TIVAGPATMEPTACVASNVYGAQSVVNLVSHGPPVSVLPBGPVHVXMGKDITLFCIS 2458
 100 SGD-----ASINVTNLQISDGTGYCKVKKAPGVGNKK 132
 2459 SGEPRSSPRWTRLGIPVKLEPRMFLMNSHAMLKIASVKPSDAGTYVCOQNALGTAQKQ 2518
 133 IQLTV---LLKPSGTRCYVDGSE---EIGNDFKLCPEKSGSLPLLEVWOKLSNOKLPT 186
 2519 VELIVDTGTVAGPTGPQVQVESELTLEAGTATLHCS-ATGNPPPTTHWSEK-----RAPL 2573
 187 LWLAEMTSPVISKVNASTESYSGTSCVTKRVRGSDQCLRLDVVPP 232
 2574 PQHRIEGNTLVIPRAVQDSGGQYICNATNSAGHTEATVVLHVESP 2619

RESULT 12
 PVRI HUMAN STANDARD; PRT; 517 AA.
 AC Q15223; Q75465; Q9HBE6; Q9HBX2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 18-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (Higr) (CD111 antigen).
 DE PVRL1 OR PRRI OR HVEC.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95237621; PubMed=7721102;
 RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C., Dubreuil P.;
 RA "cDNA characterization and chromosomal localization of a gene related to the poliovirus receptor gene.";
 RL Gene 155:261-265(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=98279152; PubMed=9616127;
 RA Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J., Spear P.G.;
 RA "Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor.";
 RT Science 280:1618-1620(1998).
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=21256041; PubMed=11356977;
 RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J., Campadelli-Fiume G., Dubreuil P.;
 RA "Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectin1 (or prr1-HvEC) modulates positively and negatively RT susceptibility to hsv infection.";
 RL J. Virol. 75:5684-5691(2001).
 RN [4]
 RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE. MEDLINE=20392396; PubMed=10932188;
 RX Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.;
 RA "Mutations of PVRL1, encoding a cell-cell adhesion RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal RT dysplasia.";
 RL Nat. Genet. 25:427-430(2000).
 CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORMS ALPHA AND DELTA) AND SECRETED (ISOFORM GAMMA).
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ALPHA, DELTA (SHOWN HERE), AND GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPEDI). It is responsible for allelic forms known as Margarita island form and Zlotogora-Ogur syndrome.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -!- DATABASE: NAME=PROV; NOTE=PROV 2.45-49(2001); WWW="http://www.ncbi.nlm.nih.gov/prov/guide/2005693930_g.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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 CC EMBL: AF197027; AAG16649.1; JOINED.
 CC EMBL: AF197028; AAG16649.1; JOINED.
 CC EMBL: AF197029; AAG16649.1; JOINED.
 CC EMBL: AF197030; AAG16649.1; JOINED.
 CC EMBL: AF197031; AAG16649.1; JOINED.
 CC EMBL: AF197032; AAG16649.1; JOINED.
 CC EMBL: AF197033; AAG16649.1; JOINED.
 CC EMBL: AF197034; AAG16649.1; JOINED.
 CC EMBL: AF197035; AAG16649.1; JOINED.
 CC EMBL: AF197036; AAG16649.1; JOINED.
 CC EMBL: AF197037; AAG16649.1; JOINED.
 CC EMBL: AF197038; AAG16649.1; JOINED.
 CC EMBL: AF197039; AAG16649.1; JOINED.
 CC EMBL: AF197040; AAG16649.1; JOINED.
 CC EMBL: AF197041; AAG16649.1; JOINED.
 CC EMBL: AF197042; AAG16649.1; JOINED.
 CC EMBL: AF197043; AAG16649.1; JOINED.
 CC EMBL: AF197044; AAG16649.1; JOINED.
 CC EMBL: AF197045; AAG16649.1; JOINED.
 CC EMBL: AF197046; AAG16649.1; JOINED.
 CC EMBL: AF197047; AAG16649.1; JOINED.
 CC EMBL: AF197048; AAG16649.1; JOINED.
 CC EMBL: AF197049; AAG16649.1; JOINED.
 CC EMBL: AF197050; AAG16649.1; JOINED.
 CC EMBL: AF197051; AAG16649.1; JOINED.
 CC EMBL: AF197052; AAG16649.1; JOINED.
 CC EMBL: AF197053; AAG16649.1; JOINED.
 CC EMBL: AF197054; AAG16649.1; JOINED.
 CC EMBL: AF197055; AAG16649.1; JOINED.
 CC EMBL: AF197056; AAG16649.1; JOINED.
 CC EMBL: AF197057; AAG16649.1; JOINED.
 CC EMBL: AF197058; AAG16649.1; JOINED.
 CC EMBL: AF197059; AAG16649.1; JOINED.
 CC EMBL: AF197060; AAG16649.1; JOINED.
 CC EMBL: AF197061; AAG16649.1; JOINED.
 CC EMBL: AF197062; AAG16649.1; JOINED.
 CC EMBL: AF197063; AAG16649.1; JOINED.
 CC EMBL: AF197064; AAG16649.1; JOINED.
 CC EMBL: AF197065; AAG16649.1; JOINED.
 CC EMBL: AF197066; AAG16649.1; JOINED.
 CC EMBL: AF197067; AAG16649.1; JOINED.
 CC EMBL: AF197068; AAG16649.1; JOINED.
 CC EMBL: AF197069; AAG16649.1; JOINED.
 CC EMBL: AF197070; AAG16649.1; JOINED.
 CC EMBL: AF197071; AAG16649.1; JOINED.
 CC EMBL: AF197072; AAG16649.1; JOINED.
 CC EMBL: AF197073; AAG16649.1; JOINED.
 CC EMBL: AF197074; AAG16649.1; JOINED.
 CC EMBL: AF197075; AAG16649.1; JOINED.
 CC EMBL: AF197076; AAG16649.1; JOINED.
 CC EMBL: AF197077; AAG16649.1; JOINED.
 CC EMBL: AF197078; AAG16649.1; JOINED.
 CC EMBL: AF197079; AAG16649.1; JOINED.
 CC EMBL: AF197080; AAG16649.1; JOINED.
 CC EMBL: AF197081; AAG16649.1; JOINED.
 CC EMBL: AF197082; AAG16649.1; JOINED.
 CC EMBL: AF197083; AAG16649.1; JOINED.
 CC EMBL: AF197084; AAG16649.1; JOINED.
 CC EMBL: AF197085; AAG16649.1; JOINED.
 CC EMBL: AF197086; AAG16649.1; JOINED.
 CC EMBL: AF197087; AAG16649.1; JOINED.
 CC EMBL: AF197088; AAG16649.1; JOINED.
 CC EMBL: AF19


```
Db 174 KPENGQYLDIYGITRDQAGEYECSEAENDVSFDDVKKVRVVNFAPTIQBIKSGVTTPGR 233
Qy 157 DFLLKCEPKESPLLYEWOK---LSNSOKLPTLMLAEMTSPVISVKNASTEYSGTYS 212
Db 234 SGLIRCE-GAGVPPAPFAFVKGKRLFNQGO-GIIIONFSTRSILVTNTQBHFNGYTC 291
Qy 213 TVNRRVSGDQCLRLDVPVPSNRAGTIAGAVIGVL-----LALVLIGLI 256
Db 292 VAANKLGTWASPLN--PFSTAQYGITGACDLFSCWSLALTSSVI 337

RESULT 14
PVRL_PIG STANDARD; PRT; 515 AA.
AC QGL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1).
GN PVRL1 OR PRRI OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
CC -1- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -1- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
CC -----
CC EMBL; AF308632; ARG30281.1;
CC HSPSP; P06907; INEU.
CC DR InterPro; IPR003599; Ig.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR InterPro; IPR003598; Ig_c2.
CC DR InterPro; IPR003600; Ig_like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 2.
CC DR SMART; SM00409; IG; 3.
CC DR SMART; SM00410; IG like; 1.
CC DR SMART; SM00408; IGc2; 2.
CC DR SMART; SM00406; IGv; 1.
CC
CC Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
KW SIGNAL
FT CHAIN 1 30
FT DOMAIN 31 515
FT FT POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT TRANSMEM 356 376
FT TRANSMEM 377 515
FT DOMAIN 44 131
FT DOMAIN 165 233
FT DOMAIN 262 323
FT DOMAIN 262 323
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FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 9.5%; Score 129.5; DB 1; Length 515;
Best Local Similarity 18.5%; Pred. No. 0.0023;
Matches 67; Conservative 50; Mismatches 86; Indels 159; Gaps 18;

Qy 34 GETAYLPCTRFTLGPEDQGLDIWLLSPADNOKVDQV-----IILYS---GDK 78
Db 44 GTDVLHCSEA-----NPLPGVKITQVTWQKATNGSKQNVAINPAMGVS 88
Qy 79 IYDDYYQDLKGRVHFTSNDLKGSDASINVTNQLSDIGTYQCKVKKAPGVNKKIQ--LT 136
Db 89 VLAPY---RERVEFLRPSFT--DGTIRLSRLEDEGVVYCFATFP--AGNRESQNL 141
Qy 137 VLLKPSGTRCYVDGSEI-----GNDFKL---KCEPKESLPLLYEWOK----- 177
Db 142 VMAKPTN--WIEGTQAVLRKAKDKDLVATCTTSANGKPPSVSVSWETHLKGEAEYQEI 198
Qy 178 -----LSNSQKLP-----TLWLAEMTSPVISVKN----- 201
Db 199 RNPNGTIVVISRYLVPSREDHRHQSLACIVNHNDRFESLTINVOYEVEVTIEGFGNW 258
Qy 202 -----ASTEY-----SGTYSCTV 214
Db 259 YLRQMDVKLTCKADANPPATEYHWTTLNGLSLPKGVEAQNRTLFRRGPIINYSMACTVCEA 318
Qy 215 KNEVSGDQCLLRLDVV-----PPSN--RAGTIAGAVIG-----VLLALVLI-GLIIFC 259
Db 319 TNPITRSGQVEVNITEFTPTSPPEHRRAGQVPTAIIGGVVGSILLVLFVVGGIIVAL 378
Qy 260 CR 261
Db 379 CR 380

RESULT 15
PGEM_HUMAN STANDARD; PRT; 4393 AA.
ID PGEM_HUMAN STANDARD; PRT; 4393 AA.
AC P98160; Q16287;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
```

RC TISSUE=Skin, and Colon;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdock A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 1018-1472 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalesky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [4]
RP SEQUENCE OF 892-1398 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to ip36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [5]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessle S., Murdock A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
CC -!- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.
CC -!- SIMILARITY: CONTAINS 22 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 SEA DOMAIN.
CC -----
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CC -----
DR EMBL; X62515; CAA44373.1; --
DR EMBL; M85289; AAA52700.1; --
DR EMBL; M64283; AAA52699.1; --
DR EMBL; S76436; AAB21121.2; --
DR EMBL; L22078; -; NOT_ANNOTATED_CDS.
DR HSSP; P00740; 1EDM.
DR Sienra-2DPAGE; P98160; --
DR Genew; HGNC:5273; HSPG2.
DR MIM; 142461; --
DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR002172; LDL_recept_A.
DR InterPro; IPR000034; Laminin_B_
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF00008; EGF_4.
DR Pfam; PF00047; ig_22.
DR Pfam; PF00052; laminin_B_3.
DR Pfam; PF00053; laminin_EGF_7.
DR Pfam; PF00054; laminin_G_3.
DR Pfam; PF00057; ldl_recept_a_4.
DR Pfam; PF01390; SEA_1.
DR PRINTS; PRO0010; EGFBL00D.
DR ProDom; PD003031; Laminin_B_3.
DR SMART; SM00180; EGF_Lam_6.
DR SMART; SM00001; EGF_like_8.
DR SMART; SM00408; IGc2_22.
DR SMART; SM00192; LDLa_4.
DR SMART; SM00281; LamB_3.
DR SMART; SM00282; LamG_3.
DR SMART; SM00200; SEA_1.
DR PROSITE; PS00022; EGF_1_9.
DR PROSITE; PS01186; EGF_2_5.
DR PROSITE; PS01248; LAMININ TYPE EGF_11.
DR PROSITE; PS00025; LAM G DOMAIN_3.
DR PROSITE; PS01209; LDLRA_1_4.
DR PROSITE; PS00668; LDLRA_2_4.
DR PROSITE; PS50024; SEA_1.
DR Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 4393 BASEMENT MEMBRANE-SPECIFIC HEPARAN
FT Sulfate PROTEOGLYCAN CORE PROTEIN.
FT DOMAIN 80 194 SEA.
FT DOMAIN 197 236 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 283 321 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 323 361 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 366 405 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 405 506 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 523 532 LAMININ EGF-LIKE 1 (N-TERMINAL).
FT DOMAIN 533 732 LAMININ DOMAIN IV 1 (DOMAIN III A).
FT DOMAIN 733 765 LAMININ EGF-LIKE 1 (C-TERMINAL).
FT DOMAIN 766 815 LAMININ EGF-LIKE 2.
FT DOMAIN 816 873 LAMININ EGF-LIKE 3.
FT DOMAIN 881 925 LAMININ EGF-LIKE 4 (INCOMPLETE).
FT DOMAIN 926 935 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 936 1127 LAMININ DOMAIN IV 2 (DOMAIN III B).
FT DOMAIN 1128 1160 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 1161 1210 LAMININ EGF-LIKE 6.
FT DOMAIN 1211 1267 LAMININ EGF-LIKE 7.
FT DOMAIN 1277 1326 LAMININ EGF-LIKE 8.
FT DOMAIN 1327 1336 LAMININ EGF-LIKE 9 (N-TERMINAL).
FT DOMAIN 1337 1531 LAMININ DOMAIN IV 3 (DOMAIN III C).
FT DOMAIN 1532 1564 LAMININ EGF-LIKE 9 (C-TERMINAL).
FT DOMAIN 1565 1644 LAMININ EGF-LIKE 10.
FT DOMAIN 1615 1672 LAMININ EGF-LIKE 11.
FT DOMAIN 1679 1773 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 1774 1867 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 1868 1957 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 1958 2053 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 2054 2153 IG-LIKE C2-TYPE DOMAIN 6.
FT DOMAIN 2154 2246 IG-LIKE C2-TYPE DOMAIN 7.
FT DOMAIN 2247 2342 IG-LIKE C2-TYPE DOMAIN 8.
FT DOMAIN 2343 2438 IG-LIKE C2-TYPE DOMAIN 9.
FT DOMAIN 2439 2535 IG-LIKE C2-TYPE DOMAIN 10.
FT DOMAIN 2536 2631 IG-LIKE C2-TYPE DOMAIN 11.
FT DOMAIN 2632 2728 IG-LIKE C2-TYPE DOMAIN 12.
FT DOMAIN 2729 IG-LIKE C2-TYPE DOMAIN 13.

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FT DOMAIN 2829 2926 IG-LIKE C2-TYPE DOMAIN 14.
FT DOMAIN 2927 3023 IG-LIKE C2-TYPE DOMAIN 15.
FT DOMAIN 3024 3114 IG-LIKE C2-TYPE DOMAIN 16.
FT DOMAIN 3115 3213 IG-LIKE C2-TYPE DOMAIN 17.
FT DOMAIN 3214 3300 IG-LIKE C2-TYPE DOMAIN 18.
FT DOMAIN 3301 3401 IG-LIKE C2-TYPE DOMAIN 19.
FT DOMAIN 3402 3490 IG-LIKE C2-TYPE DOMAIN 20.
FT DOMAIN 3491 3576 IG-LIKE C2-TYPE DOMAIN 21.
FT DOMAIN 3577 3664 IG-LIKE C2-TYPE DOMAIN 22.
FT DOMAIN 3665 3845 LAMININ G-LIKE 1.
FT DOMAIN 3846 3883 EGF-LIKE 1.
FT DOMAIN 3886 3924 EGF-LIKE 2.
FT DOMAIN 3930 4105 LAMININ G-LIKE 2.
FT DOMAIN 4106 4143 EGF-LIKE 3.
FT DOMAIN 4145 4178 EGF-LIKE 4.
FT DOMAIN 4203 4391 LAMININ G-LIKE 3.
FT SITE 65 67 HEPARAN SULFATE (POTENTIAL).
FT SITE 71 73 HEPARAN SULFATE (POTENTIAL).
FT SITE 76 78 HEPARAN SULFATE (POTENTIAL).
FT SITE 4151 4153 MEDIATES MOTOR NEURON ATTACHMENT
(POTENTIAL).
FT SITE 4301 4303 MEDIATES MOTOR NEURON ATTACHMENT
(POTENTIAL).
FT DISULFID 199 212 BY SIMILARITY.
FT DISULFID 206 225 BY SIMILARITY.
FT DISULFID 219 234 BY SIMILARITY.
FT DISULFID 285 297 BY SIMILARITY.
FT DISULFID 292 310 BY SIMILARITY.
FT DISULFID 304 319 BY SIMILARITY.
FT DISULFID 325 337 BY SIMILARITY.
FT DISULFID 332 350 BY SIMILARITY.

Query Match 9.58; Score 128.5; DB 1; Length 4393;
Best Local Similarity 23.3%; Pred. No. 0.04;
Matches 50; Conservative 35; Mismatches 75; Indels 55; Gaps 11;

Qy 20 LSITTPQMIKAKGETAYLPCRFITLGPEDQGLDIEWLLSPADNOKVDQVILYSGDKI 79
Db 3026 ISIDPSSVQ--QGQDASEK---LIHDAAPISLEW----- 3058
Qy 80 YDDYYQDLKGRVHTSNDLKGDSINVTNLQSLDICTYQCKVKAPGVGNKKIQL---- 135
Db 3059 -KTRNQELEDNVHISP-----GSIITVGTSPNHCYRCVASNAYGVAQSVVNLVHG 3112
Qy 136 --TVLLKPSGTRCYVDSGEIGNDFLKC---EPKEGSLPLLYEWQKLSNS-QKLEPTLW 188
Db 3113 PPTVSVLPEGP-VWV-----KVGKAVTLECVSAGEPRSSA-----RWTRISSTPAKLEQRT 3162
Qy 189 LAEMTS-PVISVKNASTEYSGTYSCTVKNRVGSDQ 222
Db 3163 YGLMDSHTVLIQISSAKPSDAGTVVCLAQNALGTAQ 3197

```

Search completed: July 9, 2003, 12:44:49
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 9, 2003, 12:42:53 ; Search time 32 Seconds
(without alignments)
1680.572 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359

Sequence: 1 MALLLCFVLLCGVADLTRSL.....AVIGVLLVLLGLIIFCCR 261

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | DB | ID | Description |
|------------|-------|-------|--------|----|--------|--------------------|
| 1 | 1341 | 98.7 | 319 | 6 | Q9TU79 | Q9tu79 sus scrofa |
| 2 | 1270 | 93.5 | 365 | 6 | Q8WV3 | Q8wmv3 bos taurus |
| 3 | 1254 | 92.3 | 319 | 6 | Q9TU80 | Q9tu80 canis famil |
| 4 | 1238 | 91.1 | 344 | 4 | Q9UKV4 | Q9ukv4 homo sapien |
| 5 | 1233 | 90.7 | 344 | 11 | Q9R067 | Q9r067 rattus norv |
| 6 | 1233 | 90.7 | 358 | 11 | Q9R066 | Q9r066 rattus norv |
| 7 | 1216 | 89.5 | 352 | 11 | Q9IW66 | Q9iw66 mus musculu |
| 8 | 1216 | 89.5 | 366 | 11 | Q9BEJ8 | Q9bdj8 mus musculu |
| 9 | 921 | 67.8 | 252 | 4 | Q8WWT6 | Q8wwt6 homo sapien |
| 10 | 676 | 49.7 | 200 | 4 | Q8WWT7 | Q8wwt7 homo sapien |
| 11 | 659.5 | 48.5 | 372 | 13 | Q9YV50 | Q9yv50 brachydanio |
| 12 | 641 | 47.2 | 164 | 11 | Q9YV50 | Q9y50 mus musculu |
| 13 | 378.5 | 27.9 | 373 | 4 | Q9H6B4 | Q9hb64 homo sapien |
| 14 | 366.5 | 27.0 | 373 | 11 | Q8R373 | Q8r373 mus musculu |
| 15 | 362.5 | 26.7 | 373 | 11 | Q920S5 | Q920s5 mus musculu |
| 16 | 338 | 24.9 | 89 | 4 | Q8WWT8 | Q8wwt8 homo sapien |

| | | | | | | |
|----|-------|------|------|----|--------|--------------------|
| 17 | 321.5 | 23.7 | 319 | 11 | Q922D5 | Q922d5 mus musculu |
| 18 | 311.5 | 22.9 | 319 | 11 | Q9UKA5 | Q9uka5 mus musculu |
| 19 | 301 | 22.1 | 284 | 4 | Q9NX42 | Q9nx42 homo sapien |
| 20 | 301 | 22.1 | 327 | 4 | Q96IQ7 | Q96iq7 homo sapien |
| 21 | 297 | 21.9 | 304 | 11 | Q9CVA4 | Q9cva4 mus musculu |
| 22 | 295 | 21.7 | 325 | 4 | Q9S791 | Q9s791 homo sapien |
| 23 | 291 | 21.4 | 318 | 13 | Q91664 | Q91664 xenopus lae |
| 24 | 289 | 21.3 | 328 | 11 | Q92109 | Q92109 mus musculu |
| 25 | 282 | 20.8 | 335 | 13 | Q9YGV5 | Q9ygv5 gallus gall |
| 26 | 276 | 20.3 | 335 | 13 | Q9PWR4 | Q9pwr4 gallus gall |
| 27 | 273 | 20.1 | 335 | 13 | Q9YGH1 | Q9ygh1 gallus gall |
| 28 | 255 | 18.8 | 407 | 11 | Q9D2J4 | Q9d2j4 mus musculu |
| 29 | 254 | 18.7 | 248 | 11 | Q9D0T4 | Q9d0t4 mus musculu |
| 30 | 250 | 18.4 | 259 | 4 | Q9S532 | Q9s532 homo sapien |
| 31 | 246.5 | 18.1 | 394 | 11 | Q925F2 | Q925f2 mus musculu |
| 32 | 226 | 16.6 | 390 | 6 | Q95KI3 | Q95ki3 macaca fasc |
| 33 | 217 | 16.0 | 390 | 4 | Q96T50 | Q96t50 homo sapien |
| 34 | 217 | 16.0 | 390 | 4 | Q96AP7 | Q96ap7 homo sapien |
| 35 | 195.5 | 14.4 | 181 | 13 | Q91665 | Q91665 xenopus lae |
| 36 | 188.5 | 13.9 | 300 | 11 | Q9D9J0 | Q9d9j0 mus musculu |
| 37 | 187.5 | 13.8 | 300 | 11 | Q9DA22 | Q9da22 mus musculu |
| 38 | 175.5 | 12.9 | 300 | 11 | Q9JHY1 | Q9jhy1 rattus norv |
| 39 | 171.5 | 12.6 | 298 | 11 | Q9J159 | Q9j159 mus musculu |
| 40 | 169 | 12.4 | 280 | 13 | Q9J716 | Q9j716 grus americ |
| 41 | 165 | 12.1 | 259 | 4 | Q9Y5B2 | Q9y5b2 homo sapien |
| 42 | 163.5 | 12.0 | 399 | 4 | Q9Y279 | Q9y279 homo sapien |
| 43 | 161.5 | 11.9 | 300 | 11 | Q8VC39 | Q8vc39 mus musculu |
| 44 | 159.5 | 11.7 | 4162 | 13 | Q98918 | Q98918 gallus gall |
| 45 | 159 | 11.7 | 5198 | 5 | Q96518 | Q96518 caenorhabdi |

ALIGNMENTS

RESULT 1

Q9TU79 PRELIMINARY; PRT; 319 AA.

AC Q9TU79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cocksackie-adenovirus-receptor homolog (Fragment).
GN CAR.

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=99422053; PubMed=10490761;

RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,

RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,

RA Lamers J.M.J., Poller W.;

RT "Expression of Cocksackie-adenovirus-receptor and alpha v-integrin does not correlate with adenovector targeting in vivo indicating anatomical vector barriers."

RL Gene Ther. 6:1520-1535(1999).

DR EMBL; AF109646; AAP01257.1; -.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR003600; Ig_like.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00408; IGC2; 1.

DR SMART; SM00410; IG_like; 1.

DR Immunoglobulin domain; Receptor.

FT NON TER 319

SQ SEQUENCE 319 AA; 35301 MW; C485555A6C9F1B5B CRC64;

Query Match 98.7%; Score 1341; DB 6; Length 319;

Best Local Similarity 99.2%; Pred. No. 3.2e-112;

Matches 258; Conservative 1; Mismatches 1; Indels 0; Caps 0;


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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=94422053; PubMed=10490761;
RA Fechner H., Haack A., Wang X., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109643; AAF01254.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 344 344
SQ SEQUENCE 344 AA; 38097 MW; BEF3722E96C697AA CRC64;

Query Match 91.1%; Score 1238; DB 4; Length 344;
Best Local Similarity 89.3%; Pred. No. 6.4e-103;
Matches 233; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKSGSLPLLVEWQKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKSGSLPLLVEWQKLSN 180
QY 181 SOKLPTLWLAEMTSPVISVKNASSTGYSTCTVKNRVGSDQCLLRLLDVVPPSNRAGTIA 240
DB 181 SOKMPTSLWLAEMTSPVISVKNASSTGYSTCTVKNRVGSDQCLLRLLDVVPPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 261
DB 241 GAVIGVLLALVLIIGLIIFCCR 261

RESULT 5
Q9R067 ID Q9R067 PRELIMINARY; PRT; 344 AA.
AC Q9R067;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Coxsackie-adenovirus-receptor homolog (Fragment).
GN CAR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=LIVER;
RX MEDLINE=94422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109644; AAF01255.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 358 358
SQ SEQUENCE 358 AA; 39261 MW; 731B7384A786BB04 CRC64;

not correlate with adenovector targeting in vivo indicating anatomical
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RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109643; AAF01254.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 344 344
SQ SEQUENCE 344 AA; 38030 MW; D436498820D8B9B7 CRC64;

Query Match 90.7%; Score 1233; DB 11; Length 344;
Best Local Similarity 89.6%; Pred. No. 1.8e-102;
Matches 233; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADLTRSLITTPPEOMIEKAGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
DB 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQLSDIGTYQC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKSGSLPLLVEWQKLSN 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEBEIGNDFKLCPEKSGSLPLLVEWQKLSN 180
QY 181 SOKLPTLWLAEMTSPVISVKNASSTGYSTCTVKNRVGSDQCLLRLLDVVPPSNRAGTIA 240
DB 181 SOKMPTSLWLAEMTSPVISVKNASSTGYSTCTVKNRVGSDQCLLRLLDVVPPSNRAGTIA 240
QY 241 GAVIGVLLALVLIIGLIIFCCR 260
DB 241 GAVIGVLLALVLIIGLIIFCCR 260

RESULT 6
Q9R066 ID Q9R066 PRELIMINARY; PRT; 358 AA.
AC Q9R066;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Coxsackie-adenovirus-receptor homolog (Fragment).
GN CAR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=LIVER;
RX MEDLINE=94422053; PubMed=10490761;
RA Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultzeiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers."
RL Gene Ther. 6:1520-1535 (1999).
DR EMBL; AF109644; AAF01255.1; -.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00410; IG like; 1.
KW Immunoglobulin domain; Receptor.
FT NON_TER 358 358
SQ SEQUENCE 358 AA; 39261 MW; 731B7384A786BB04 CRC64;

not correlate with adenovector targeting in vivo indicating anatomical
```

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Query Match      90.7%; Score 1233; DB 11; Length 358;
Best Local Similarity 89.6%; Pred. No. 1.9e-102;
Matches 233; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAGETAYLPCRTLTGDPDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADFTSLITTPQRIEKAGETAYLPCRTLTGDPDQGLDIEWLLS 60

QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDKSGDASINVTNLQSLDGTGYQC 120
DB 61 PSDNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDKSGDASINVTNLQSLDGTGYQC 120

QY 121 KVKAPGVGNKKIQTLLVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLYEWOKLSN 180
DB 121 KVKAPGVGNKKIQTLLVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLYEWOKLSN 180

QY 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRSGDQCLLRDLVVPPSNRAGTIA 240
DB 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRSGDQCLLRDLVVPPSNRAGTIA 240

QY 241 GAVIGVLLALVLGLIIFCC 260
DB 241 GAVIGVLLALVLGLIIFCC 260

RESULT 7
Q91W66 PRELIMINARY; PRT; 352 AA.
AC Q91W66;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Cxsackievirus and adenovirus receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fuhunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK004908; BAB23660.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 352 AA; 38843 MW; 2BD8CBD25D8CE123 CRC64;

Query Match      89.5%; Score 1216; DB 11; Length 352;
Best Local Similarity 88.1%; Pred. No. 6.3e-101;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAGETAYLPCRTLTGDPDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADFTSLITTPQRIEKAGETAYLPCRTLTGDPDQGLDIEWLLS 60

QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDKSGDASINVTNLQSLDGTGYQC 120
DB 61 PSDNQIYDQVILYSGDKIYDDYQDLKGRVHFTSNDKSGDASINVTNLQSLDGTGYQC 120

QY 121 KVKAPGVGNKKIQTLLVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLYEWOKLSN 180
DB 121 KVKAPGVGNKKIQTLLVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLYEWOKLSN 180

QY 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRSGDQCLLRDLVVPPSNRAGTIA 240
DB 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRSGDQCLLRDLVVPPSNRAGTIA 240

QY 241 GAVIGVLLALVLGLIIFCC 260
DB 241 GAVIGVLLALVLGLIIFCC 260
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RESULT 8
Q9DBJ8 PRELIMINARY; PRT; 366 AA.
AC Q9DBJ8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Cxsackievirus and adenovirus receptor.
GN CXADR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fuhunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK004908; BAB23660.1; -.
DR MGD; MGI:1201679; Cxadr.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00410; IG_Like; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 366 AA; 40078 MW; D1C3CA7163F3B231 CRC64;

Query Match      89.5%; Score 1216; DB 11; Length 366;
Best Local Similarity 88.1%; Pred. No. 6.6e-101;
Matches 229; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAGETAYLPCRTLTGDPDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADFTSLITTPQRIEKAGETAYLPCRTLTGDPDQGLDIEWLLS 60

QY 61 PADNOKVDQVILYSGDKIYDDYQDLKGRVHFTSNDKSGDASINVTNLQSLDGTGYQC 120
DB 61 PSDNQIYDQVILYSGDKIYDDYQDLKGRVHFTSNDKSGDASINVTNLQSLDGTGYQC 120

QY 121 KVKAPGVGNKKIQTLLVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLYEWOKLSN 180
DB 121 KVKAPGVGNKKIQTLLVLLKPSGTRCYVDGSEIIGNDFKLKCPKSGSLPLLYEWOKLSN 180

QY 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRSGDQCLLRDLVVPPSNRAGTIA 240
DB 181 SOKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRSGDQCLLRDLVVPPSNRAGTIA 240

QY 241 GAVIGVLLALVLGLIIFCC 260
DB 241 GAVIGVLLALVLGLIIFCC 260
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RESULT 9
Q8WWT6 PRELIMINARY; PRT; 252 AA.
AC Q8WWT6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cocksackie-adenovirus-receptor isoform CAR4/7.
CXADR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dornier A., Xiong D., Yajima T., Knowlton K.U.;
RT "A soluble coxsackie adenovirus receptor is elevated in Cocksackie B3
RT infected mice.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072912; AAL68890.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
KW Receptor.
SQ SEQUENCE 252 AA; 28201 MW; 4532559D01AB67E2 CRC64;

Query Match 67.8%; Score 921; DB 4; Length 252;
Best Local Similarity 83.4%; Pred. No. 1.2e-74;
Matches 176; Conservative 8; Mismatches 13; Indels 14; Gaps 1;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQSLDITYQC 120
DB 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQSLDITYQC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCEPKESGLPLLYEW 180
DB 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCEPKESGLPLLYEW 180
QY 181 SOKLPTLTLA-----EMTSPVI 197
DB 181 SQKMTSWLAGKCHLQRAVRPLPEATSAVI 211

RESULT 10
Q8WWT7 PRELIMINARY; PRT; 200 AA.
AC Q8WWT7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cocksackie-adenovirus-receptor isoform CAR3/7.
CXADR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dornier A., Xiong D., Yajima T., Knowlton K.U.;
RT "A soluble coxsackie adenovirus receptor is elevated in Cocksackie B3
RT infected mice.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072911; AAL68879.1; -.
DR InterPro; IPR003599; IG.
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DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_like; 1.
KW Receptor.
SQ SEQUENCE 200 AA; 22370 MW; 43FDB19DF6A7FEB8 CRC64;

Query Match 49.7%; Score 676; DB 4; Length 200;
Best Local Similarity 75.4%; Pred. No. 8.8e-53;
Matches 132; Conservative 12; Mismatches 19; Indels 12; Gaps 2;

QY 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRFTLGPEDQGLDIEWLLS 60
DB 1 MALLLCFVLLCGVADLTRSLITTPQMIKAKGETAYLPCRFTLGPEDQGLDIEWLLS 60
QY 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQSLDITYQC 120
DB 61 PADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQSLDITYQC 120
QY 121 KVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCEPKESGLPLLYEW 175
DB 121 KVKKAPGVGNKKIHLVVL-----GKMC HLQRA-----VRPLPEATSAVIHPW 163

RESULT 11
Q90Y50 PRELIMINARY; PRT; 372 AA.
AC Q90Y50;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cocksackie virus and adenovirus receptor-like protein.
GN CAR.
OS Brachydanio rerio (Zebrafish) (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20535037; PubMed=11080637;
RA van Raaij M.J., Chouin E., van der Zandt H., Bergelson J.M.,
RA Cusack S.;
RT "Dimeric structure of the coxsackievirus and adenovirus receptor D1
RT domain at 1.7 A resolution.";
RL Structure 8:1147-1155(2000).
DR EMBL; AF268197; AAKS8592.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
KW Receptor.
SQ SEQUENCE 372 AA; 40664 MW; C363B71E7601C73A CRC64;

Query Match 48.5%; Score 659.5; DB 13; Length 372;
Best Local Similarity 45.8%; Pred. No. 6.5e-51;
Matches 121; Conservative 57; Mismatches 73; Indels 13; Gaps 3;

QY 3 LLLCFVLL-----CGVADLTRSLIT-TPEOMIEKAKGETAYLPCRFTLGPEDQGLDIE 56
DB 8 LCYVYVLLTGSACG-----LQITSTGQTSIEKASGESVKLDCQFTLASDGSGLDIE 60
QY 57 WLLSPADNQKVDQVILYSGDKIYDDYQDLKGRVHFTSNDLKS GDASINVTNLQSLDITG 116
DB 61 WSLQPSDNQKEKQVIVYSGDRAFEHYDPLKGRVHFNPSDPKNGDASNNIMGLKATDITG 120
QY 117 TYQCKVKKAPGVGNKKIQLTVLLKPSGTRCYVDGSEIIGNDFKLKCEPKESGLPLLYEW 176
DB 121 TYQCKIKVPGIARSKYLLTMVVRPSKPKCSAEGQTYVGKVMVLCSSVEGTPQMEYIWE 180
QY 177 KLSNQKPLTLMAEMTSPVIVSKVASTEYSGTCTVKNRVCSGDOCLLRDLQVWPPSNRA 236
DB 181 RTSGNKLPLPLAILDKVGTGTLTKNATGASGTGRCQAKNRVGTGECVVEVTITQPNTA 240
```


Db 199 MASSGLYQCTAGNEAGKESCVVRV-TVQYVQSIGMWAGAVTGIVAGALLIFLLIW 252

RESULT 15

Q920S5 PRELIMINARY; PRT; 373 AA.
AC Q920S5; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Adipocyte-specific protein 5.
GN ASP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsuruga H.;
RT "Adipocyte-specific protein 5, a novel protein upregulated during
RT adipocyte differentiation.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040490; BAB68503.1;
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00047; I9; 2.
SQ SEQUENCE 373 AA; 41186 MW; 5C6280584AF95326 CRC64;

Query Match 26.7%; Score 362.5; DB 11; Length 373;
Best Local Similarity 34.9%; Pred. No. 3.1e-24;
Matches 82; Conservative 48; Mismatches 96; Indels 9; Gaps 5;
QY 29 IEKAGGETAYLPCRFTLGPEDQGLDTEWLLSPADNQVDQVILYSGDKIYDDYQDLK 88
Db 22 IKRVAEEKVTLPCHHQLGLPEKOTLDIEWLLT--DNEGKQKVITYSSRHVYNNLTTEEOK 79
QY 89 GRVHFTSNDLKSGDASINVTNLOLSDIGTYQCKVKAPGVGNKKIQLTVLLKPSGTRCYV 148
Db 80 GRVAFASNFL-AGDASLQIEPLKPSDEGRYTCVKQNSGRYVWVSHVILKALVRPSKPKCEL 138
QY 149 DGSEETGNDPKLCEPKESGLPLLYEWOKL---SNSOKLPTLWLAEMTSP-VISVKNAS 203
Db 139 EGEPTGSDTLQCESASGKPIVYVWQRIREKEGEDEHLPPKSRIDYNNPGRVLLQNL 198
QY 204 TEYSGTYSCTVKNRVGSQCLRLDLVVPVPSNRAGTIAGAVIGVLLALVLIIGLIIF 258
Db 199 MASSGLYQCTAGNEAGKESCVVRV-TVQYVQSIGMWAGAVTGIVAGALLIFLLIW 252

Search completed: July 9, 2003, 12:45:29
Job time : 34 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 11:13:22 ; Search time 1878 Seconds

(without alignments)
4044.639 Million cell updates/sec

Title: US-09-899-634c-2

Perfect score: 1359
Sequence: 1 MALLLCFVLGCVADLTRSL.....AVIGVLALVLGLIIFCCR 261

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spool/US0989634/runat.09072003.11138.16343/app_query.fasta.1.455
-DB=GenEmbl -OPMT=fscap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdt -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:.*
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2: gb_hcg.*
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6: gb_pat.*
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33: em_hcg_mus.*
34: em_hcg_pin.*
35: em_hcg_rtd.*
36: em_hcg_mam.*
37: em_hcg_vrt.*
38: em_sy.*
39: em_hcg_hum.*
40: em_hcg_mus.*
41: em_hcg_other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|------------------------------|
| 1 | 1341 | 98.7 | 959 | 4 | AF109646 Sus scrofa |
| 2 | 1270 | 93.5 | 1184 | 4 | AY033651 Bos taurus |
| 3 | 1254 | 92.3 | 959 | 4 | AF109645 Canis fam |
| 4 | 1238 | 91.1 | 1033 | 9 | AF124598 Homo sapi |
| 5 | 1238 | 91.1 | 2354 | 9 | HSU90716 U90716 Human cell |
| 6 | 1238 | 91.1 | 2434 | 6 | ARI57886 ARI57886 Sequence |
| 7 | 1238 | 91.1 | 2434 | 9 | HS46KDA Y07593 H.sapiens m |
| 8 | 1238 | 91.1 | 2537 | 9 | BC010536 BC010536 Homo sapi |
| 9 | 1238 | 91.1 | 2537 | 9 | BC003684 BC003684 Homo sapi |
| 10 | 1238 | 91.1 | 3060 | 6 | AX055476 AX055476 Sequence |
| 11 | 1238 | 91.1 | 3060 | 6 | AX089948 AX089948 Sequence |
| 12 | 1238 | 91.1 | 3060 | 6 | AX358962 AX358962 Sequence |
| 13 | 1238 | 91.1 | 3060 | 6 | AX362455 AX362455 Sequence |
| 14 | 1238 | 91.1 | 3060 | 6 | AX403617 AX403617 Sequence |
| 15 | 1238 | 91.1 | 3060 | 6 | AX454694 AX454694 Sequence |
| 16 | 1238 | 91.1 | 3060 | 6 | AX491172 AX491172 Sequence |
| 17 | 1238 | 90.7 | 1376 | 6 | AX098210 AX098210 Sequence |
| 18 | 1233 | 90.7 | 1376 | 10 | AF109643 AF109643 Rattus no |
| 19 | 1233 | 90.7 | 1076 | 10 | AF109644 AF109644 Rattus no |
| 20 | 1224 | 90.1 | 1095 | 6 | ARI44703 ARI44703 Sequence |
| 21 | 1224 | 90.1 | 1584 | 6 | ARI44702 ARI44702 Sequence |
| 22 | 1216 | 89.5 | 1098 | 10 | NMCARH Y10320 M.musculus |
| 23 | 1216 | 89.5 | 1206 | 10 | NMCARH U90715 Mus musculus |
| 24 | 1216 | 89.5 | 1515 | 6 | ARI44704 ARI44704 Sequence |
| 25 | 1216 | 89.5 | 1669 | 10 | NMCARH Y11929 M.musculus |
| 26 | 1216 | 89.5 | 1696 | 10 | NMCARH BC016457 Mus musculus |
| 27 | 1145 | 84.3 | 170558 | 2 | AC012414 AC012414 Homo sapi |
| 28 | 1145 | 84.3 | 1522 | 9 | HSW805355 AL834140 Homo sapi |
| 29 | 1133 | 83.4 | 108122 | 2 | AC116905 AC116905 Homo sapi |
| 30 | 1131 | 83.2 | 167605 | 2 | AC068446 AC068446 Homo sapi |
| 31 | 1131 | 83.2 | 174104 | 2 | AC060814 AC060814 Homo sapi |
| 32 | 1103.5 | 81.2 | 152318 | 2 | AL162851 AL162851 Homo sapi |
| 33 | 1103.5 | 81.2 | 166239 | 9 | HS214614 AL050303 Homo sapi |
| 34 | 1103.5 | 81.2 | 340000 | 9 | HS21C004 AL163204 Homo sapi |
| 35 | 921 | 67.8 | 759 | 9 | AY072912 AY072912 Homo sapi |
| 36 | 875 | 64.4 | 64976 | 2 | AC026256 AC026256 Homo sapi |
| 37 | 676 | 49.7 | 603 | 9 | AY072911 AY072911 Homo sapi |
| 38 | 659.5 | 48.5 | 1883 | 5 | AF268197 AF268197 Danio rer |
| 39 | 641 | 47.2 | 1312 | 10 | BC004680 BC004680 Homo sapi |
| 40 | 407 | 29.9 | 1296 | 9 | AB079879 AB079879 Homo sapi |
| 41 | 402.5 | 29.6 | 1905 | 9 | BC034411 BC034411 Homo sapi |
| 42 | 400.5 | 29.5 | 1287 | 10 | AB079880 AB079880 Mus muscu |
| 43 | 378.5 | 27.9 | 2307 | 9 | BC009371 BC009371 Homo sapi |
| 44 | 378.5 | 27.9 | 2458 | 6 | AX358876 AX358876 Sequence |
| 45 | 378.5 | 27.9 | 2458 | 6 | AX362369 AX362369 Sequence |

RESULT 1

ALIGNMENTS

| LOCUS | AF109646 | 599 bp | MRNA | linear | MAM 06-OCT-1999 |
|---|--|--------|------|--------|-----------------|
| DEFINITION | Sus scrofa coxsackie-adenovirus-receptor homolog (CAR) mRNA, | | | | |
| ACCESSION | AF109646 | | | | |
| VERSION | AF109646.1 | | | | |
| KEYWORDS | GI:6013138 | | | | |
| SOURCE | Sus scrofa. | | | | |
| ORGANISM | Sus scrofa. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. | | | | |
| REFERENCE | 1 (bases 1 to 959) Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Lamers,J.M.J. and Polner,W. Expression of coxsackie adenovirus receptor and alpha-v-integrin does not correlate with adenovector targeting in vivo indicating anatomical vector barriers Gene Ther. 6 (9), 1520-1535 (1999) | | | | |
| AUTHORS | Schoemaker,R., Veghel,R., Houtsmille,A., Schultzeiss,H.P., Lamers,J. and Polner,W. | | | | |
| TITLE | Expression of coxsackie adenovirus receptor and alpha-v-integrin does not correlate with adenovector targeting in vivo indicating anatomical vector barriers Gene Ther. 6 (9), 1520-1535 (1999) | | | | |
| JOURNAL | 99422053 | | | | |
| MEDLINE | 10490761 | | | | |
| PubMed | 2 (bases 1 to 959) | | | | |
| REFERENCE | Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Lamers,J.M.J. and Polner,W. | | | | |
| AUTHORS | Submitted (25-NOV-1998) Department of Cardiology and Pneumology, Benjamin Franklin University Hospital, Hindenburgdamm 30, Berlin 12200, Germany | | | | |
| TITLE | Location/Qualifiers | | | | |
| JOURNAL | 1..959 /organism="Sus scrofa" /db_xref="taxon:9823" /tissue_type="liver" 1..>959 /gene="CAR" 1..>959 /gene="CAR" /codon_start=1 /product="coxsackie-adenovirus-receptor homolog" /protein_id="AAF01257.1" /db_xref="GI:6013139" /translation="MALILRFVLIQGVADLRSLSTTPPEOMIEKAGETAYLPSCRPT LGPEPDGPDLEMLSPADKNQVLIILYSGDKTYDDYDLKGRPHNLSKSDP ASIVNTNQLSDIGTYQCKVKAPSGVGNKKIQLVLKPSSTRCYVGSEIINDFKL KCEDEGSLPLLYEMQKLSNQKLPTMLAMTSPVSVKNASTEYSGETYVKNVW GSDCELRIDVPPSNRAGTITAGAVITGLVLAIVLIGLIVFCCHKRRREKEKEVHHND IREVDPPEKSRSTARSYLGSNHSLSGMSPSNMGSKTYQYN" | | | | |
| FEATURES | BASE COUNT 290 a 200 c 219 g 250 t | | | | |
| ORIGIN | 290 a 200 c 219 g 250 t | | | | |
| Alignment Scores: | Pred. No.: 4.14e-123 Length: 959 Score: 1341.00 Matches: 258 Percent Similarity: 99.62% Conservative: 1 Best Local Similarity: 99.23% Mismatch: 1 Query Match: 98.68% Indels: 0 Gaps: 0 | | | | |
| US-09-899-634C-2 (1-261) X AF109646 (1-959) | | | | | |
| OY | 1 MetAlaLeuLeuLeuCySPhyVaIleuLeuCySgIyVaIaIaAspLeuThArgSerIeu 20 | | | | |
| Db | 1 ATGGGCGCTTCGCTGCGCTCGCTGCTCGTGTGGAGTCGCGGATCTCACAGAAATTGG 60 | | | | |
| OY | 21 SerIeThrrrrPrroGluGlnMetIleGluIysAlaIysGlyGluThAlaTyrrLeuPro 40 | | | | |
| Db | 61 AGTACCTACTCTCCGAAACAAGTATTAAGGCAAGGCGAAAGGCGAATCTATTTGGCG 120 | | | | |
| OY | 41 CysArgPheThrLeuGlyPrroGluAspGlnGlyProLeuAspIleGluTrpLeuLeuSer 60 | | | | |
| Db | 121 TGCAGATTATCCCTGGCTCCAGAGACCAAGGGGCGCGCTGGACATCGATGCTGCTGCA 180 | | | | |
| OY | 61 ProAlaAspAengInLysValaIaSpGlnValIleIleLeuTyrSerGlyAspLysIleTy 80 | | | | |

[illegible]

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/translation="MELLRLRLRLALGVAFPMRGLSTTPPEMIKAKGETAYLPCKET
US-09-899-634C-2 (1-261) x AY033651 (1-1184)

Alignment Scores:
Pred. No.: 5,47e-116 Length: 1184
Score: 1270.00 Matches: 242
Percent Similarity: 95.77% Conservative: 7
Best Local Similarity: 93.08% Mismatch: 11
Query Match: 93.45% Indels: 0
DB: 4 Gaps: 0

BASE COUNT 346 a 274 c 279 g 285 t
ORIGIN

QY 1 MetLaleuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db 1 ATGAGAGCTTCTGCTGGCGCTTCTTCTGCTGCGGAGTGGGGATTTTCCACAGAGGCTTG 60
QY 21 SerLeuThrThrProGluGluMetLleGluLysAlaLysGlyValuThAlaTyrLeuPro 40
Db 61 AGTATCACTACTCTCCGAAACAGATGATTAAGAGCAAGGGGAAATCGTTATTGGCA 120
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspLleGluThrLeuLeuSer 60
Db 121 TGCAAATTTACCCTGGCGTCCGGAAGCCAGGGGCTCTGACATGATGCTGCTGCA 180
QY 61 ProAlaAspAsnGlnLysValAspGlnValLleLeuTyrSerGlyAspLysLleTyr 80
Db 181 CCACCTGATTAATCGAAGGTGATCAAGTGAATTAATTATTTATTCGAGACAAATTTAT 240
QY 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
Db 241 GATGACTRACTRTCAGACCTGAAAGACGAGTACATTTTCAAGTAAGATCTCAAAATCT 300
QY 101 GlyAspAlaSerLleAsnValThrAsnLeuGlnLeuSerAspLleGluThrTyrGlnCys 120
Db 301 GGTGATGCTTCAATTAATGATGACAAATTTACGCTGACAGTATTTGGCACATATCAGTGC 360
QY 121 LysValLysLysAlaProGlyValGlyAsnLysLysLleGlnLeuThrValLeuLeuLys 140
Db 361 AAAGTGAAAAAAGCTCCTGGTGTGGAAATTAAGATTACGCTGACAGTCTTGTGTAAG 420
QY 141 ProSerGlyThrArgCysValThrValAspLysSerGluGluLleGlyAsnAspPheLysLeu 160
Db 421 CTTTCAAGTATACAGATGTTATGATGATGATCAGAAAGAAATTTGGAAAGACCTTAATCTC 480
QY 161 LysCysGluProLysGlnGlySerLeuProLeuLeuTyrGluThrPglLysLeuSerAsn 180
Db 481 AAATGTGAACCAAAAGAAAGTTCACCTCCACATGATGATGATGATGATGATGATGATGAT 540
QY 181 SerGlnLysLeuProThrLeuThrLeuAlaGluMetThrSerProValLleSerValLys 200
Db 541 TCACAGAAACAGCCACCTCTTGTTGTTACAGAGAAATGACATACCTGTTATATCTGTGAAA 600
QY 201 AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
Db 601 AATGCCAATGCCGAAATCTCCGGAGACATACCTGTATGAGTATGAGTATGAGTATGAGTAT 660
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrLleAla 240
Db 661 GATCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 241 GlyAlaValLleGlyValLeuLeuAlaLeuValLeuLleGlyLeuLleLlePheCys 260
Db 721 GGAGCTGTTAAGGAACCTTGTGCGGCTTGTGCTTATGCTTATGCTTATGCTTATGCTTATGCT 780

```

| RESULT 3 | AFI09645 | 959 bp | mRNA | linear | MAM 06-OCT-1999 |
|---|---|---------------|------|--------|-----------------|
| LOCUS | AFI09645 | | | | |
| DEFINITION | Canis familiaris coxsackie-adenovirus-receptor homolog mRNA, | | | | |
| ACCESSION | AFI09645 | | | | |
| VERSION | AFI09645.1 | GI:6013136 | | | |
| KEYWORDS | | | | | |
| SOURCE | Canis familiaris. | | | | |
| ORGANISM | Canis familiaris | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. | | | | |
| AUTHORS | 1 (bases 1 to 959) Fechner,H., Haack,A., Wang,H., Wang,X., Eizema,K., Pauschinger,M., Schoemaker,R., Vegheli,R., Houtsmuller,A., Schultzeis,H.P., Lamers,J. and Poller,W. | | | | |
| TITLE | Expression of coxsackie adenovirus receptor and alphav-integrin does not correlate with adenovector targeting in vivo indicating anatomical vector barriers | | | | |
| JOURNAL | Gene Ther. 6 (9), 1520-1535 (1999) | | | | |
| MEDLINE | 99422053 | | | | |
| PUBMED | 10490761 | | | | |
| REFERENCE | 2 (bases 1 to 959) Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Lamers,J.M.J. and Poller,W. | | | | |
| AUTHORS | Direct Submission | | | | |
| TITLE | Submitted (24-NOV-1998) Department of Cardiology and Pneumology, Benjamin Franklin University Hospital, Hindenburgdamm 30, Berlin 12200, Germany | | | | |
| JOURNAL | | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1..959 /organism="Canis familiaris" /strain="Breed German shepherd" /db_xref="taxon:9615" /tissue_type="liver" 1..>959 /codon_start=1 /product="coxsackie-adenovirus-receptor homolog" /protein_id="AA01256.1" /db_xref="GI:6013137" /translation="MALILRFVLLCGVADTRLSLITTPQMIERAKGETAYLPCKFTT LSBEDQDPLDEMLSPADQAKQDOVILISGKIYDDYQDLKGRVHFTSNDKSGD ASINVTILRLSDIGTQCKYKAGVGNKIIQTLTVKPSGICVYGSSSEIGNDFKL KCPKESGLPLOYEMOKLSNOKTPRMSDTPSVISINASREYGTICVTNWKV GSPQCCRLNWWPSPNRAGTIAAGVGIILALVIGTIVYCCCKRREKREKVVHND IREVPEPLKRTSTARSYSIGNSHSLGSMSPSMNEGYSKTYQN" | | | | |
| CDS | | | | | |
| BASE COUNT | 300 a 201 c 206 g 252 t | | | | |
| ORIGIN | | | | | |
| Alignment Scores: | | | | | |
| Pred. NO.: | 1.59e-114 | Length: | 959 | | |
| Score: | 1254.00 | Matches: | 238 | | |
| Percent Similarity: | 94.64% | Conservative: | 9 | | |
| Best Local Similarity: | 91.19% | Mismatches: | 14 | | |
| Query Match: | 92.27% | Indels: | 0 | | |
| DB: | 4 | Gaps: | 0 | | |
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| QY | 1 MetAlaLeuLeuLeuLeuCySPhenAlLeuLeuCySgLYValAlaAspLeuThrArgSerLeu 20 | | | | |
| Db | 1 ATGGCGGTCTCTGCTGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60 | | | | |
| QY | 21 SerLeThrThrProGluGlnMetIleGluLeuLeuAlaLeuGlyGluThrAlaTyrLeuPro 40 | | | | |
| Db | 61 AGTATCTACTACTCTCTGAACAGATGATTGAAGAAGGCCAAAGGGGGAACCTGCTTATTGCCA 120 | | | | |
| QY | 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluThrPleLeuSer 60 | | | | |
| Db | 121 TGCAAATTTCCTTAAGTCAGAGACCAAGGACCGCTTGACATCGAGTGCGCTCTGTCA 180 | | | | |
| QY | 61 ProAlaAspAsnGlnValaAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80 | | | | |

| Db | 181 | CCAGCTGATTAATCAAGAAAGTGGACCAAGTGAATTATTTATTTATTTCTTCGACAGACAAATTTAT | 240 |
|------------|----------|---|---|
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| Db | 241 | GACGCCTACTCTCAAGATCTGAAAGACAGACATTTTAAACGAAAGAACTCAAACT | 300 |
| Qy | 101 | GLyAsPaLaSer1LeAsnValThrsemlenglnleuSerAsp1LeGlyThrTyGlnCys | 120 |
| Db | 301 | GGTATGATCATCATTAATGTAACCAATTTACGGTTGTGATGATTTGGACATACCAAGTC | 360 |
| Qy | 121 | LySValLySlySaLaPProGlyValGlyAsnLySly1LeGlnLeuThrValleuLeuLyS | 140 |
| Db | 361 | AAAGGAAAAAAGCTCGTGGTGGATTAAGAATTCAGCTGACAGTCTTGTTAG | 420 |
| Qy | 141 | ProSerGlyThrArgCysTyTValAspGlySerGluGlu1LeGlyAsnAspPheyleu | 160 |
| Db | 421 | CCTTCAGGTATTAAGATGTTAGCTGATGATGATCAGAAAGAAATGGAAAGACTTTAACTA | 480 |
| Qy | 161 | LySCysGluPProLyGluGlySerleuProleuLeuTyrgluTrpGlnLyLeuSerAsn | 180 |
| Db | 481 | AAATGTGAACCAAAAGAAAGTTCACTTCCATTACATATGAATGGCAAAAATGTCCAT | 540 |
| Qy | 181 | SerGlnLySleuProThrleuTrleuValagluMetThrSerProVal1LeSerValLyS | 200 |
| Db | 541 | TCACAGAAAAGCCCCCTCGGTGCAACAGATTAAGACTTCACTCGTTATATCTATAAA | 600 |
| Qy | 201 | AsnAlaSerThrGluTyrSerGlyThrTySerCysThrValLySaenArValGlySer | 220 |
| Db | 601 | AATGCCTCTACTGACTACTCTGGGACATACATCTGTACAGTAACAAACCGAGTAGGCTCT | 660 |
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| Db | 661 | GATCAGTCCACGACTACGCTGATATTTGTTCCACCTTAATAGAGCTGGAAACANTGCA | 720 |
| Qy | 241 | GLyAlaVal1LeGlyValleuLeuAlaLeuValleu1LeGlyLeu1LePheCysCys | 260 |
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| Qy | 261 | Arg 261 | |
| Db | 781 | CGT 783 | |
| RESULT 4 | | | |
| LOCUS | AF124598 | 1033 bp | mRNA linear PRI 29-SEP-1999 |
| DEFINITION | | | Homo sapiens coxsackie and adenovirus receptor protein (HCAR2) |
| ACCESSION | | | AF124598 |
| VERSION | | | AF124598.1 GI:4884701 |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | Homo sapiens. |
| REFERENCE | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS | | | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| TITLE | | | 1 (bases 1 to 1033) |
| JOURNAL | | | Rechner,H., Haack,A., Wang,H., Wang,X., Eizema,K., Pauschinger,M., |
| MEDLINE | | | Schoemake,R., Veghel,R., Houtsmuller,A., Schultheiss,H.P., |
| PUBMED | | | Lamers,J. and Poller,W. |
| REFERENCE | | | Expression of coxsackie adenovirus receptor and alphaV-integrin |
| AUTHORS | | | does not correlate with adenovector targeting in vivo indicating |
| | | | anatomical vector barriers |
| | | | Gene Ther. 6 (9), 1520-1535 (1999) |
| | | | 99422053 |
| | | | 10490761 |
| | | | 2 (bases 1 to 1033) |
| | | | Fechner,H., Haack,A., Wang,H., Wang,X., Wiese,A., Lamers,J.M.J. and |
| | | | Poller,W. |
| | | | Direct Submission |
| | | | Submitted (29-JAN-1999) Department of Cardiology and Pneumology, |
| | | | Benjamin Franklin Hospital, Hindenburgdamm 30, Berlin 12200, |
| | | | Germany |
| FEATURES | | | Location/Qualifiers |
| source | | | 1..1033 |

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Qy 241 G1yAlaValIleGlyValLeuLeuAlaLeuValIleGlyLeuIleIlePheCysCys 260
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Qy 261 Arg 261
Db 781 CGT 783
RESULT 5
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DEFINITION Human cell surface protein HCAR mRNA, complete cds.
ACCESSION U90716
VERSION U90716.1 GI:1946350
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Tomko, R.P., Xu, R. and Philipson, L.
TITLE HCAR and MCR: the human and mouse cellular receptors for subgroup C adenoviruses and group B coxsackieviruses
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (7), 3352-3356 (1997)
MEDLINE 97250541
PUBMED 9096397
REFERENCE 2 (bases 1 to 2354)
AUTHORS Tomko, R.P., Xu, R. and Philipson, L.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-1997) Structural Biology, Skidball Institute for Biomolecular Medicine, New York University Medical Center, 550 First Avenue, New York, NY 10016, USA
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location/Qualifiers
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/note="Immunoglobulin superfamily member"
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BASE COUNT 709 a 417 c 471 g 757 t
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Alignment Scores:
Pred. No.: 1 87e-112 Length: 2354
Score: 1238.00 Matches: 233
Percent Similarity: 94.25% Conservative: 13
Best Local Similarity: 89.27% Mismatches: 15
Query Match: 91.10% Indels: 0
DB: 9 Gaps: 0
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Db 1 ATGGCCCTCTGCTGTGCTTCCGCTCTGTGGGAGTGTGATTTCCCGCAAGCTTG 60
Qy 21 SerIleThrThrProGluInMeCIIleGluValAlaValGlyGluThrAlaTrpLeuPro 40
Db 61 AGATACACTACTCTCTGAAGAGATGATGTAAGAAAGCAAGGGAAATCCTATCTGCCG 120
Qy 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGlyTrpLeuLeuSer 60
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Qy 61 ProAlaAspAsnGlnValValAspGlnValIleIleLeuTrpSerGlyAspIleTrp 80
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Qy 261 Arg 261
Db 781 CGT 783
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LOCUS AR157886 2434 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6245966.
ACCESSION AR157886
VERSION AR157886.1 GI:16218903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2434)
TITLES Degregori, J.
JOURNAL Adenoviral mediated gene transfer into lymphocytes
Patent: US 6245966-A 1 12-JUN-2001;
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QY      121 LysValIleLysAlaProGlyValAlaGlyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
Db      420 AAAGTGAATAAAAGCTCTGCTGTTGCAATAAAGAAATTCATCTGTAGTTCTTTAG 479
QY      141 ProSerGlyThrArgCysTyTyrValaAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
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QY      161 LysCysGluProLysGluGlySerLeuProLeuLeuTyGluTyrGlnLysLeuSerAsn 180
Db      540 AATGTGAACCAAAAGAGTTCACCTTCATTCAGTATGAGTGGCAAAATGTCTGAC 599
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QY      221 ASPGlnCysLeuLeuArgLeuAspValAlaProProSerAsnArgAlaGlyThrIleAla 240
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RESULT 8
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LOCUS      Homo sapiens, coxsackie virus and adenovirus receptor, clone
ACCESSION      MGC:17118 IMAGE:345544, mRNA, complete cds.
VERSION      BC010536.1 GI:14714774
KEYWORDS      MGC.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 2447)
AUTHORS      Strausberg, R.
TITLE      Direct Substitution
JOURNAL      Submitted (10-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
Email: cgsabrs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Huiyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

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ORIGIN

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Score:      1238.00      Matches:      233
Percent Similarity:      94.25%      Conservative:      13
Best Local Similarity:      89.27%      Mismatches:      15
Query Match:      91.10%      Indels:      0
DB:      9      Gaps:      0

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QY      61 ProAlaAspAsnGlnLysValaAspGlnValIleLeuTyrSerGlyAspLysIleTyr 80
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>
 Series: IRAX Plate: 19 Row: F Column: 7
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503112.

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QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
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QY 181 SerGlnLysLeuProThrThrLeuTyrPleuAlaGluMetThrSerProValIleSerValLys 200
DB 616 TCACAGAAATGCGCCATTCATGTTAGCAGAAATGCTTCATCTGTTAATATCTGTAATA 675
QY 201 AsnAlaSerThrGlnTyrSerGlyTyrThrSerCysThrValLysAsnArgValGlySer 220
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DB 796 GGAGCATTATAGAACCTTGTGCTGCTAGCCGCTCATTTGCTTATCATCTTTTGTGT 855
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RESULT 9
LOCUS BC003684 2537 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, coxsackie virus and adenovirus receptor, clone
ACCESSION MGC:5086 IMAGE:3463613, mRNA, complete cds.
VERSION BC003684.1 GI:13277551
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Bkaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 2537)
JOURNAL Strausberg, R.
Direct Submission
Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL),
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
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BASE COUNT 809 a 458 c 509 g 761 t
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Alignment Scores:
Pred. No.: 2,06e-112 Length: 2537
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Percent Similarity: 94.25% Conservative: 13
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Query Match: 91.10% Indels: 0
DB: 9 Gaps: 0
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| DEFINITION | Sequence 106 from Patent WO0073452. | | |
| ACCESSION | AX055476 | | |
| VERSION | AX055476.1 | | |
| KEYWORDS | GI:12228735 | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| AUTHORS | 1 (bases 1 to 3060) Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tamas, D., Watanabe, C.K. and Wood, W.I. | | |
| TITLE | Compositions and methods for the treatment of immune related diseases | | |
| JOURNAL | Patent: WO 0073452-A 106 07-DEC-2000; | | |
| FEATURES | Genetech, Inc. (US) | | |
| source | Location/Qualifiers | | |
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| BASE COUNT | 1094 a 559 c 569 g 837 t | 1 | others |
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| QY | 41 | CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrPheLeuSer | 60 |
| Db | 197 | TGCCAATTTCAGCTTAGTCCCGAAGACCGGACCGCTGACATCGAGTGGCTGATATCA | 256 |
| QY | 61 | ProAlaAspAsnGlnIuYsValAspGlnValIleIleLeuTrYserGlyAspIuYsIleYr | 80 |
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| QY | 81 | AspAspTrYTrYcGlnAspLeuIuYsGlyArgValHisPheThrSerAsnAspLeuYsSer | 100 |
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| Db | 377 | GGTGAATGCATCAATTAATGTTAAGCAATTTTACACTCTCGATTTGGCACATATCAGTGC | 436 |
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| Dd | | 617 | TCAAGAAAATGCCCATCTCATGGTAGCGAATAATGACTTCATCTGTAATATCTGAATA | 676 |
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| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| REFERENCE | 1 (bases 1 to 3060) | | | |
| AUTHORS | Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Tumas,D., | | | |
| | Watanabe,C.K. and Wood,W.I. | | | |
| TITLE | Compositions and methods for the treatment of immune related diseases | | | |
| JOURNAL | Patent: WO 0116319-A 9 08-MAR-2001; | | | |
| FEATURES | Genentech, Inc. (US) | | | |
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| BASE COUNT | 1094 a 559 c 569 g 837 t | 1 others | | |
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ACCESSION      AX358962
VERSION      AX358962.1 GI:18675382
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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Patent: WO 0193983-A 215 13-DEC-2001;
JOURNAL      Genentech Inc. (US)
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BASE COUNT      1094 a      559 c      569 g      837 t      1 others
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Score:      1238.00      Matches:      233
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Best Local Similarity:      89.27%      Mismatches:      15
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      Db      137 AGTATCATCTCTCTGAAAGATGATTTGAAAAAGCCAAAGGGGAAATCTCATTTGCCA 196
      QY      41 CysArgPheThrLeuGlyProGlnuSpGlnGlyProLeuAsp11egluTYrPLeuLeuSer 60
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LOCUS      AX362455
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ACCESSION      AX362455
VERSION      AX362455.1 GI:18694685
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| | Mammalia; Eutheria; Primates; Catarrhini; Hominiina; Hominidae; Homo. | | | |
| REFERENCE | | | | |
| AUTHORS | Ashtkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Geyrhofer,M., Goddard,A., Godowski,P., Grimaldi,C.D., Gunney,A.L., Kljavin,I., Napier,M.A., Pan,J., Pooni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.I. and Zhang,Z. The same Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent : WO 0073454-A 504 07-DEC-2000; Genentech Inc. (US) | | | |
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| OY | 41 | CysArghethrlEuglyProgluaSPGLngLYProleuaspIlegutTPleuLeuSer | 60 | |
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| OY | 61 | ProblaaspaengInLyVaLaSPGNvalIllelleuuryfserGlYAapLyLIeTyR | 80 | |
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| OY | 101 | GLYaAPlaaserllEasnvaIThrasnleuGlnLeusearapiileglyThrytYrgInCys | 120 | |
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GenCore version 5.1.6
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| 27 | 378.5 | 27.9 | 2458 | 20 | AAZ33941 |
| 28 | 378.5 | 27.9 | 2458 | 21 | AACT8473 |
| 29 | 378.5 | 27.9 | 2458 | 21 | AAAC5595 |
| 30 | 378.5 | 27.9 | 2458 | 22 | AA521437 |
| 31 | 378.5 | 27.9 | 2458 | 22 | AAAF44262 |
| 32 | 378.5 | 27.9 | 2458 | 24 | ABL95892 |
| 33 | 378.5 | 27.9 | 2458 | 24 | ABL88103 |
| 34 | 375.5 | 27.6 | 1948 | 22 | AAAC84415 |
| 35 | 367.5 | 27.0 | 1949 | 22 | AAAC84417 |
| 36 | 366.5 | 27.0 | 1122 | 22 | AAAC84392 |
| 37 | 366.5 | 27.0 | 1949 | 22 | AAAC84416 |
| 38 | 366.5 | 27.0 | 1949 | 22 | AAAC84416 |
| 39 | 363.5 | 26.7 | 1949 | 22 | AAAC84418 |
| 40 | 362.5 | 26.7 | 1927 | 22 | AAH76376 |
| 41 | 357 | 26.3 | 811 | 22 | ABA06752 |
| 42 | 357 | 26.3 | 811 | 22 | AA528873 |
| 43 | 351.5 | 25.9 | 2865 | 18 | AAAT62369 |
| 44 | 351.5 | 25.9 | 2793 | 22 | AAH57436 |
| 45 | 351.5 | 25.9 | 2793 | 22 | AAAF44988 |

ALIGNMENTS

RESULT 1
AAV50429
ID AAV50429 standard; cDNA; 2354 BP.
XX AAV50429;
AC AAV50429;
XX
DT 07-DEC-1998 (first entry)
XX
DE Human coxsackievirus and Ad2 and Ad5 receptor (HCAR) cDNA.
XX
KW HCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
KW Ad5 receptor; human; infection; vaccine; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH
FT
Key CDS Location/Qualifiers
1..1098
/*tag= a

| | |
|------------------------|-----------|
| Alignment Scores: | |
| Pred. No.: | 1,056-121 |
| Score: | 1224.00 |
| Percent Similarity: | 93.87% |
| Best Local Similarity: | 88.89% |
| Query Match: | 90.07% |
| DB: | 19 |
| | |
| Length: | 1589 |
| Matches: | 232 |
| Conservative: | 13 |
| Mismatches: | 16 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-899-634C-2 (1-261) x AAV28845 (1-1584)

| | | | |
|----|-----|--|-----|
| QY | 1 | MetAlaIeuleuLeuCySHeValIeuleuCyGsiGlyValAlaAspIeuthrArgSerLeu | 20 |
| Db | 60 | ATGGCCCTCCTGCTGGCTTCGTCGCTCCCTGTCGGAGTAGAGGATTTCGCCAGAAAGTTTG | 119 |
| QY | 21 | SerIleThrProGluInMetIleGlyValAlaGsiGlyValThrAlaTyrLeuPro | 40 |
| Db | 120 | AGATCACTACTCTCTGAAGAGATGATGAAAAAGCCAAAGGGGAAACGCTTACTTCGCG | 179 |
| QY | 41 | CysArgPheThrLeuGlyProGluAspGlnGlyProAlaAspIleGluTyrLeuLeuSer | 60 |
| Db | 180 | TGCAAAATTTACGCTTAAGTCCCGAGACCGAGACCGCTGACATCGAGTGGCTATATCA | 239 |
| QY | 61 | ProAlaAspAsnGlnValAspGlnValIleIleLeuTyrSerGlyAspIleTyr | 80 |
| Db | 240 | CCAGCTGATATACAGAAAGGTGGATCAAGATATTATTATTCGAGGACAAATTTAT | 239 |
| QY | 81 | AspAspTyrTyrGlnAspLeuGsiGlyArgValHisPheThrSerAsnAspLeuLysSer | 100 |
| Db | 300 | GATGACTACTATCCAAATCTGAAGAGCCGAGATCAATTTTACAGAAATGATCTCAAAATCT | 359 |
| QY | 101 | GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys | 120 |
| Db | 360 | GGGATGATCACTAAATATGATGAAGATTTTACAACGTGATGATGGACATATCAATGTC | 419 |
| QY | 121 | LysValIleLysValaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLys | 140 |
| Db | 420 | AAAGTGAATAAAAGCTCTGCTGTTGCAATTAAGAAATCCATCTGATGTTCTTGTTAAG | 479 |
| QY | 141 | ProSerGlyThrArgCysTyrValaAspGlySerGluGluIleGlyAsnAspPheLysLeu | 160 |
| Db | 480 | CTTTCAAGGTGCGAGATGTTACGTGATGATGATCTGAAGAAATGGAGAAGCACTTTAAGATA | 539 |
| QY | 161 | LysGsiGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn | 180 |
| Db | 540 | AAATGTGAACCAAAAGAAAGGTTCACTTCATTACAGTATGAGTGGCAAAAATTTGTCGAC | 599 |
| QY | 181 | SerGlnLysLeuProThrLeuThrLeuIleAsnIleGluMetThrSerProValIleSerValLys | 200 |
| Db | 600 | TCACAGAAATATGCCCACTTCATCGTTAGAGAAATGACTCATCTGTTATATCTGTAAAA | 659 |
| QY | 201 | AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValaGlySer | 220 |
| Db | 660 | AAATGCTCTTCTGAGTACTCTGGAGCATACACTGTACGTACGAACAGAGTGGCTCT | 719 |
| QY | 221 | AspGlnCysLeuLeuArgLeuAspValaProProSerAsnArgAlaGlyThrIleAla | 240 |
| Db | 720 | GATCAGTGCCTGTTGGGTCTAAACGTGTCTCTCTTCAAAATAAAGCTGAGCTAATTGCA | 779 |
| QY | 241 | GlyValaValIleGlyValLeuLeuAlaLeuValIleGlyLeuIleIlePheCysCys | 260 |
| Db | 780 | GGAGCCATATATAGAACTTTGCTGCTCAGCGCTCATGTCCTTATCATCTTTTGCTGT | 839 |
| QY | 261 | Arg | 261 |
| Db | 840 | CGT | 842 |

RESULT 13
ID AAV28846 standard; DNA: 1128 BP.
NC AAV28846;
XX

| | | |
|-----|--|---|
| DT | 03-AUG-1998 | (first entry) |
| XX | | |
| DE | Mouse | coxsaackievirus and adenovirus receptor encoding DNA. |
| XX | | |
| KW | Mouse; coxsackievirus; adenovirus; receptor; CAR; cardiac infection; | |
| KW | myocarditis; pericarditis; dilated cardiomyopathy; meningoencephalitis | |
| KW | pancreatic infection; acute pancreatitis; gastrointestinal tract; | |
| KW | diabetes mellitus; ss. | |
| XX | | |
| OS | Mus sp. | |
| XX | | |
| Key | Location/Qualifiers | |
| FH | 1..1128 | |
| FT | CDS | |
| FT | /*tag= a | |
| FT | /product= "coxsaackievirus and adenovirus receptor" | |
| FT | /transl_except= (pos:1096..1098,aa:Yaa) | |
| FT | /note= "Yaa= a stop codon, the sequence is shown as | |
| FT | continuing but gets unclear" | |

PS Disclosure; Fig 14; 104pp; English.

XX

CC The present sequence encodes mouse coxsackievirus and adenovirus receptor (CAR). The present invention also describes: (1) a method for CC modulating CAR expression comprising contacting the cell with an agent CC which modulates CAR protein activity or CAR nucleic acid expression, CC such that a cell associated activity is altered relative to a cell CC associated activity of the cell in the absence of the agent; and (2) a CC method for detecting the presence of CAR in a biological sample CC comprising contacting a biological sample with an agent capable of CC detecting CAR protein or mRNA such that the presence of CAR is detected. CC Modulation of CAR is useful for treatment of cardiac infection, e.g. CC myocarditis, pericarditis or dilated cardiomyopathy, or infection of the CC central nervous system, e.g. a non-specific febrile illness or CC meningoencephalitis, or pancreatic infection, e.g. acute pancreatitis, CC or infection of the respiratory or gastrointestinal tract or childhood CC onset diabetes mellitus. Probes derived from CAR nucleic acids are CC useful for hybridization assays, and antibodies raised against CAR CC protein are useful for blocking CAR expression. Cell-free assays which CC include combining CAR protein and a candidate/test compound are useful CC in screening for drugs which interact with CAR protein.

XX

XX Sequence 1128 BP; 297 A; 286 C; 288 G; 257 T; 0 other;

XX

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 4,76e-121 | Length: | 1128 |
| Score: | 1216.00 | Matches: | 229 |
| Percent Similarity: | 93.85% | Conservative: | 15 |
| Best Local Similarity: | 88.08% | Mismatches: | 16 |
| Query Match: | 89.48% | Indels: | 0 |
| DB: | 19 | Gaps: | 0 |

US-09-839-634C-2 (1-261) x AAV28846 (1-1128)

0Y 1 MetAlaIeUdeUeUcYSpheValIeUeUcYGylValAlaAspIeuThraIrgSerIeu 20

```

Db      1 ATGGCCGGCCTACTGCTGCTTGTGCTTGTGGCGGATCGCGGATTTCCACAGTGGTTG 60
QY      21 Ser1eThrThrProgluInMeT1eGlulysAlaYsG1uThrAlaTYrLeuPro 40
Db      61 AGCATCACTACACCCGACAGAGATGCAAAAAGCCAAAGGGAACTGGTATCTTACCA 120
QY      41 CysArgPheThrLeuGlyProgluAspGlnGlyProLeuAsp11eGluTrpLeuLeuSer 60
Db      121 TGCAGATTACTCTCAGCTCCGCAAGACGAGGACCACTGACATTTGAATGCTGATATTC 180
QY      61 ProAlaAspAsnGlnYsValaAspGlnVal11e1eLeuTYrSerG1yAsp11eTYr 80
Db      181 CCTCTGATTAACAGATAGTGATCAAGTATATTTGATTTCTGGAGCAAAATTTAT 240
QY      81 AspAspTYrTYrGlnAspLeuYsG1yArGValH1sPheThrSerAsnAspLeuYsSer 100
Db      241 GATTACTACTATCCGATCTGAAAGACGGGTACATTTTCAGTAAACGATGTCACGTCT 300
QY      101 GlyAspAlaSer11eAsnVal1ThrAsnLeuGlnLeuSerAsp11eGlyThrTYrGlnCys 120
Db      301 GGGAGCGCATCTATAATGATGACCAACCTGCACTGCGACATTGGCACTTACCAAGTGC 360
QY      121 LysVal11eLysAlaProG1yValG1yAsnLysLys11eGlnLeuThrValLeuLeuYs 140
Db      361 AAAGTGAAAGAACCCCTGGGGGTTGCAAAATAGAAATTCCTGCTGACCCGTTCTTTAG 420
QY      141 ProSerG1yThrArgCysTYrValaAspG1ySerG1uGln11eG1yAsnAspPheLysLeu 160
Db      421 CCTTCAGTACAAAGATCTTCGTGATGATCGGAGAGATTGGAAATGACTTCAAGCTA 480
QY      161 LysCysGlnProLysG1uG1ySerLeuProLeuLeuTYrG1uTrpGlnYsLeuSerAsn 180
Db      481 AAATGTGAAGCCAAAGAGAGCTCCCTCCACTACAGTTGAATGCGAGAAATGTCGAGAC 540
QY      181 SerGlnLysLeuProThrLeuTrpLeuAlaGlnMeThrSerProVal11eSerValYs 200
Db      541 TCCCAAGCATGCTTACGCGCATGCTGGCAGAAATGACGACCATATATCTGTGAGAG 600
QY      201 AsnAlaSerThrGlnTYrSerG1yThrTYrSerCysThrValYsAsnArGValG1ySer 220
Db      601 AAGCCAGCTTCTAGTATTTCTGGACATACAGCTGCGACGGTTCAAAACAGATGGGCTCT 660
QY      221 AspGlnCysLeuLeuArgLeuAspVal1ValProProSerAsnArgAlaG1yThr11eAla 240
Db      661 GACCAAGTGTATGCTGGCAGTACAGCTGTCTCCACCTCCCAACGAGCGGAGAGATCGCG 720
QY      241 GlyAlaVal11eG1yValLeuLeuAlaLeuVal11eG1yLeu11e1ePheCysCys 260
Db      721 GGGCGCTGTATAGGAGCGCTGCTGGCCCTGTGCTCATCGGGGCGCATCTTCTGCTGT 780

```

RESULT 14

AAVS0430
ID AAVS0430 standard; cDNA, 1301 BP.

XX AAVS0430;
XX AC
XX DT 07-DEC-1998 (first entry)

XX Mouse coxsackievirus and Ad2 and Ad5 receptor (MCAR) cDNA.

XX MCAR; coxsackievirus receptor; CVB; adenovirus; Ad2 receptor;
XX Ad5 receptor; mouse; infection; vaccine; gene therapy; ds.

XX Mus sp.

XX Key Location/Qualifiers
XX FT 157..1215
XX CDS /*tag= a

XX MO9833819-A1.

XX 06-AUG-1998.

XX

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PF      30-JAN-1998; 98WO-US01724.
XX      30-JAN-1997; 97US-0036986.
PR      (UYNV ) UNIV NEW YORK STATE.
XX      Philipson L, Tomko RP;
XX      MPI; 1998-437397/37.
XX      P-PSDB; AAM69698.
DR      DNA encoding human receptor for adenovirus C and coxsackievirus B -
PT      for preventing and treating viral infection and rendering cells
PT      susceptible to transformation by adenoviral vectors in gene therapy
XX      Claim 2; Page 68-70; 88pp; English.
XX      This cDNA molecule codes for mouse MCAR protein (see AAM69698) that
XX      serves as a cellular receptor for adenoviruses of the serotypes 2
XX      and 5 (subgroup C) and for the group B coxsackieviruses (CVB). It
XX      was obtained by screening a lambda phage expression cDNA library
XX      with antiserum containing antibodies specific for mouse CVB
XX      binding protein p46, and was used to identify human HCAR cDNA
XX      (see AAVS0429). The invention also provides host cells transformed
XX      with DNA molecules encoding HCAR or MCAR and methods of producing
XX      the recombinant proteins or their derivatives. These proteins,
XX      CC their extracellular domains, as well as oligopeptides (see
XX      CC AAM69699-708) which bind virus, are also provided. Isolated HCAR or
XX      CC MCAR proteins or their fragments or variants are used to prevent
XX      CC or treat virus infections. Expressing the DNA in cells which lack
XX      CC these viral receptors renders the cells susceptible to
XX      CC transformation by adenoviral vectors carrying genes for gene
XX      therapy.
SQ      Sequence 1301 BP; 355 A; 327 C; 322 G; 297 T; 0 other;

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Alignment Scores:

Pred. No.: 5.8e-121 Length: 1301
Score: 1216.00 Matches: 229
Percent Similarity: 93.85 Conservative: 15
Best Local Similarity: 88.08 Mismatches: 16
Query Match: 89.48 Indels: 0
DB: 19 Gaps: 0

US-09-899-634c-2 (1-261) x AAVS0430 (1-1301)

```

QY      1 MetAlaLeuLeuLeuLeuCysPheVal11eLeuLeuCysG1yValAlaAspLeuThrArgSerLeu 20
Db      157 ATGGCCGGCCTACTGCTGCTTGTGCTTGTGGCGGATCGCGGATTTCCACAGTGGTTG 216
QY      21 Ser1eThrThrProgluInMeT1eGlulysAlaYsG1uThrAlaTYrLeuPro 40
Db      217 AGCATCACTACACCCGACAGAGATGCAAAAAGCCAAAGGGAACTGGTATCTTACCA 276
QY      41 CysArgPheThrLeuGlyProgluAspGlnGlyProLeuAsp11eGluTrpLeuLeuSer 60
Db      277 TGCAGATTACTCTCAGCTCCGCAAGACGAGGACCACTGACATTTGAATGCTGATATTC 336
QY      61 ProAlaAspAsnGlnYsValaAspGlnVal11e1eLeuTYrSerG1yAsp11eTYr 80
Db      337 CCTCTGATTAACAGATAGTGATCAAGTATATTTGATTTCTGGAGCAAAATTTAT 396
QY      81 AspAspTYrTYrGlnAspLeuYsG1yArGValH1sPheThrSerAsnAspLeuYsSer 100
Db      397 GATTACTACTATCCGATCTGAAAGACGGGTACATTTTCAGTAAACGATGTCACGTCT 456
QY      101 GlyAspAlaSer11eAsnVal1ThrAsnLeuGlnLeuSerAsp11eGlyThrTYrGlnCys 120
Db      457 GGGAGCGCATCTATAATGATGACCAACCTGCACTGCGACATTGGCACTTACCAAGTGC 516
QY      121 LysVal11eLysAlaProG1yValG1yAsnLysLys11eGlnLeuThrValLeuLeuYs 140
Db      517 AAAGTGAAAGAACCCCTGGGGGTTGCAAAATAGAAATTCCTGCTGACCCGTTCTTTAG 576

```

```

QY 141 ProSerGlyThrArgCysTyrValAspGlySerGluIleGlyAsnAspPheLysLeu 160
DB 577 CCTTCAGGTACCAAGATGCTTCGGATGGATCCGAAGAGATTGGAAATGACTTCAAGCTA 636
QY 161 LysCGluProLysGluGlySerLeuProLeuLeuTyrGluTrpGluLysLeuSerAsn 180
DB 637 AAATGTGAACCCAAAGGAGGCTCCCTTCCACTCAGTTTAAATGGCGAAACGTGTGGAC 696
QY 181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValLys 200
DB 697 TCCCAAGACATGCTTACGCGCATGGCTGGCGAAATGACGTCACAGTTATATCTGTGAAG 756
QY 201 AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
DB 757 AACGCCAGTCTGTAGTATCTGTGGACATACAGCTGCACGGTTCAAAACAGAGTGGGCTCT 816
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
DB 817 GACCAAGTATGCTGCGACTAGACGTTGTCCACCCCTCCAAACGAGCCGGAACGATCGCG 876
QY 241 GlyAlaValIleGlyValLeuLeuAlaLeuValIleGlyLeuIleIlePheCysCys 260
DB 877 GGGCGCTCATAGGAGCGCTGCTGGCCCTTGTGCTCATCGGGCGCATCTCTTGTGCTGT 936

RESULT 15
AAV72025
ID AAV72025 standard; DNA; 795 BP.
XX
AC AAV72025;
XX
DT 29-MAR-1999 (first entry)
XX
DE Adenovirus PACTSG2-SCAR DNA.
XX
KW PACTSG2-SCAR; chimeric protein; adenoviral fibre protein; monomer;
KM trimerisation domain; affinity; substrate; gene therapy vector;
XX attachment; interaction assay; infection; ss.
XX
OS Mastadenovirus.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..795
FT /*tag= a
FT /product= "PACTSG2-SCAR"
FT /note= "chimeric protein"
XX
PN MO9854346-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98MO-US11024.
XX
PR 16-JAN-1998; 98US-0071668.
XX
PR 28-MAY-1997; 97US-0047849.
XX
PA (GENV-) GENVEC INC.
XX
PI Brough DE, Einfeld D, Kovesi I, Lizonova A, Roelink PW,
PI Wickham TJ, Yonehiro G;
XX
DR WPI; 1999-059848/05.
XX
DR P-PSDB; AAM82729.
XX
PT New adenoviral fibre trimer with reduced binding to native substrate
PT useful for, e.g. preparing gene therapy vector with minimal
PT ectopic infection for in vitro applications
XX
PS Example 8; Page 58-59; 103pp; English.
XX
CC This sequence encodes a novel adenovirus chimeric protein, PACTSG2-SCAR.
CC This protein is used in a method for the construction of novel monomers

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CC having an N-terminus of an adenoviral fibre protein and a trimerisation
CC domain. Such monomers have lower affinity for native substrate than the
CC native adenoviral fibre trimer. Cell lines containing such monomers are
CC used (i) to propagate adenovirus for use as gene therapy vectors (for in
CC vitro or in vivo applications, (ii) as reagents for studying adenoviral
CC attachment and infection, and (iii) in receptor-ligand interaction
CC assays. The new viruses produce minimal ectopic infection (they can not
CC infect native host cells) so are safer as vectors and can be engineered
CC for selective targeting to other cells.
XX
SO Sequence 795 BP; 236 A; 157 C; 191 G; 211 T; 0 other;

Alignment Scores:
Pred. No.: 2,67e-113 Length: 795
Score: 1142.00 Matches: 214
Percent Similarity: 94.63% Conservative: 15
Best Local Similarity: 86.43% Mismatches: 13
Query Match: 84.03% Indels: 0
DB: 20 Gaps: 0

US-09-899-634c-2 (1-261) x AAV72025 (1-795)
QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
DB 1 ATGGCGCTCTCTGTGCTTCTGCTGCTCTGCTGCGAGTGTGGATTTCCCGAAGTTTG 60
QY 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyGluThrAlaTyrLeuPro 40
DB 61 AGTATCACTACTCTCTAAGAGATGATGTAAGAAAGCCAAAGGGGAATCTGCTGCGCC 120
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTrpLeuLeuSer 60
DB 121 TCGAATTTCACGCTGTAGTCCCGAAGACAGGAGCCGCTGACATCAGTGGCTGATATCA 180
QY 61 ProAlaAspAsnGlnLysValAspGlnValIleLeuTyrSerGlyAspLysIleTyr 80
DB 181 CCAAGCTGAATACAGAGGTGATCAAGTATTATTTATTTGGAACAATAATTTAT 240
QY 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
DB 241 GATGACTACTATCCAGATCTGAAGGCCAGATTCATTATTCAGATATGATCTCAATCT 300
QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
DB 301 GGTGATGATCAATATAATGTAACGAATTTACAACGTCTGAGATATGGACATATCAGTGC 360
QY 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
DB 361 AAAGTGAAAAAGCTCTGCTGTGTCGAAATTAAGAAATTCATCTGTGTTAAG 420
QY 141 ProSerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
DB 421 CCTTCAGGTGCGAGATGTTACGTTGATGATCTGAAGAAATGGAGATGACTTTAAGATA 480
QY 161 LysCGluProLysGluGlySerLeuProLeuLeuTyrGluTrpGluLysLeuSerAsn 180
DB 481 AAATGTGAACCAAAAGAGTTCATCTTCATTACAGTACAGTACGCAAAATATGCTGCAC 540
QY 181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValLys 200
DB 541 TCACAGMAAATGCGCCACTCATGTTAGCAGAAATACCTTCACTCTGTATATCTGTAAAA 600
QY 201 AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
DB 601 AATGCTCTTCTGAGTACTGTGGACATACAGCTACAGTACGAAACAGAGTGGCTCT 660
QY 221 AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
DB 661 GATCAGTGCCTGTGTGCTTAAACGTTGTCCCTTCAATATAAAGCTGATCTGATCC 720
QY 241 GlyAla 242
DB 721 GGCTCA 726

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Wed Jul 16 14:24:18 2003

us-09-899-634c-2.rng

Page 16

Search completed: July 12, 2003, 12:09:32
Job time : 194 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 12:03:42 ; Search time 45 Seconds
(without alignments)
1778.725 Million cell updates/sec

Title: US-09-899-634c-2

Perfect score: 1359
Sequence: 1 MALLICFVLLCGVADLTSL.....AVIGVLLALVILGILFFCCR 261

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|---------------------|
| 1 | 1238 | 91.1 | 2434 | US-09-272-496-1 | Sequence 1, Appl1 |
| 2 | 1224 | 90.1 | 1095 | US-08-928-383B-3 | Sequence 3, Appl1 |
| 3 | 1224 | 90.1 | 1584 | US-08-928-383B-1 | Sequence 1, Appl1 |
| 4 | 1216 | 89.5 | 1515 | US-08-928-383B-25 | Sequence 25, Appl1 |
| 5 | 351.5 | 25.9 | 960 | US-08-597-4958-23 | Sequence 23, Appl1 |
| 6 | 351.5 | 25.9 | 960 | US-09-068-051A-23 | Sequence 23, Appl1 |
| 7 | 351.5 | 25.9 | 2565 | US-08-597-4958-29 | Sequence 29, Appl1 |
| 8 | 351.5 | 25.9 | 2565 | US-09-068-051A-31 | Sequence 31, Appl1 |
| 9 | 351.5 | 25.9 | 2793 | US-09-336-536-68 | Sequence 33, Appl1 |
| 10 | 351.5 | 25.9 | 2803 | US-09-068-051A-63 | Sequence 68, Appl1 |
| 11 | 301.5 | 22.2 | 2184 | US-09-484-970B-131 | Sequence 161, Appl1 |
| 12 | 258 | 19.0 | 2166 | US-09-175-928-1 | Sequence 1, Appl1 |

| | | | | | |
|----|-------|------|------|-------------------|---------------------|
| 13 | 246.5 | 18.1 | 1182 | US-09-336-536-38 | Sequence 38, Appl1 |
| 14 | 246.5 | 18.1 | 1846 | US-09-336-536-37 | Sequence 37, Appl1 |
| 15 | 217 | 16.0 | 1387 | US-08-979-424-2 | Sequence 2, Appl1 |
| 16 | 202 | 14.9 | 1831 | US-09-484-970B-84 | Sequence 84, Appl1 |
| 17 | 196 | 14.4 | 1140 | US-09-462-270-1 | Sequence 1, Appl1 |
| 18 | 196 | 14.4 | 1421 | US-09-188-930-254 | Sequence 254, Appl1 |
| 19 | 191 | 14.1 | 1421 | US-09-188-930-70 | Sequence 70, Appl1 |
| 20 | 190 | 14.0 | 1110 | US-09-336-536-27 | Sequence 27, Appl1 |
| 21 | 190 | 14.0 | 1869 | US-09-336-536-26 | Sequence 26, Appl1 |
| 22 | 181.5 | 13.4 | 1295 | US-09-254-465A-8 | Sequence 8, Appl1 |
| 23 | 178.5 | 13.1 | 1022 | US-09-152-060-35 | Sequence 35, Appl1 |
| 24 | 163.5 | 12.0 | 1744 | US-09-484-970B-83 | Sequence 83, Appl1 |
| 25 | 163.5 | 12.0 | 2181 | US-09-254-465A-7 | Sequence 7, Appl1 |
| 26 | 163.5 | 12.0 | 2181 | US-09-254-465A-11 | Sequence 11, Appl1 |
| 27 | 158 | 11.6 | 752 | US-09-430-503-19 | Sequence 19, Appl1 |
| 28 | 158 | 11.6 | 752 | US-09-430-503-23 | Sequence 23, Appl1 |
| 29 | 157.5 | 11.6 | 1009 | US-09-462-270-3 | Sequence 3, Appl1 |
| 30 | 156 | 11.5 | 752 | US-09-430-503-17 | Sequence 17, Appl1 |
| 31 | 156 | 11.5 | 752 | US-09-430-503-21 | Sequence 21, Appl1 |
| 32 | 155 | 11.4 | 1151 | US-09-430-503-3 | Sequence 3, Appl1 |
| 33 | 155 | 11.4 | 1151 | US-09-430-503-5 | Sequence 5, Appl1 |
| 34 | 155 | 11.4 | 1151 | US-09-430-503-7 | Sequence 7, Appl1 |
| 35 | 154 | 11.3 | 921 | US-08-184-009-202 | Sequence 202, Appl1 |
| 36 | 154 | 11.3 | 921 | US-08-458-356-202 | Sequence 202, Appl1 |
| 37 | 154 | 11.3 | 921 | US-08-460-735-202 | Sequence 202, Appl1 |
| 38 | 153 | 11.3 | 1151 | US-09-430-503-1 | Sequence 1, Appl1 |
| 39 | 149 | 11.0 | 1716 | US-08-147-772-3 | Sequence 3, Appl1 |
| 40 | 149 | 11.0 | 1716 | US-08-456-104-7 | Sequence 7, Appl1 |
| 41 | 149 | 11.0 | 1716 | US-08-101-624-24 | Sequence 24, Appl1 |
| 42 | 149 | 11.0 | 1716 | US-08-153-262-3 | Sequence 3, Appl1 |
| 43 | 149 | 11.0 | 1716 | US-08-479-744A-30 | Sequence 30, Appl1 |
| 44 | 149 | 11.0 | 1716 | US-08-280-757B-10 | Sequence 30, Appl1 |
| 45 | 149 | 11.0 | 1716 | US-09-159-135-3 | Sequence 3, Appl1 |

ALIGNMENTS

RESULT 1
US-09-272-496-1
; Sequence 1, Application US/09272496
; Patent No. 6245966
; GENERAL INFORMATION:
; APPLICANT: Degrexi, James
; TITLE OF INVENTION: Adenoviral mediated gene transfer into lymphocytes
; FILE REFERENCE: 90-98
; CURRENT APPLICATION NUMBER: US/09/272,496
; EARLIER FILING DATE: 1999-03-19
; EARLIER APPLICATION NUMBER: US 60/092782
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (60)..(1154)
US-09-272-496-1

Alignment Scores:

Pred. No.: 7,3e-144
Score: 1238.00
Percent Similarity: 94.25%
Best Local Similarity: 89.27%
Query Match: 91.10%
DB: 4
Length: 2434
Matches: 233
Conservative: 13
Mismatch: 15
Indels: 0
Gaps: 0

US-09-899-634c-2 (1-261) x US-09-272-496-1 (1-2434)

QY 1 MetAlaLeuLeuLeuCySphValLeuLeuCySgIyValAlaAspLeuThraArgSerLeu 20
DB 60 ATGGGCGCTCTGCTGCTTCCGTCGAGTAGTGAGATTTCGCCAGAGATTG 119

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QY      21 Ser11eThrThrProGluGlnMet11eGluValAlaValGlyGluThrAlaTyrLeuPro 40
      120 AGTATCACTACTCTCTGAGAGAGATGATTGAAGAAAGCCAAAGGGGAAACTGCTTATCTGCCG 179
QY      41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAsp11eGluTyrPLeuLeuSer 60
      180 TGCMAATTATACGCTGATGCTCCGGAAGACCAAGGAGCCGCTGACATCGAGTGGCTGATATCA 239
QY      61 ProAlaAspAsnGlnValAspGlnVal11eLeuTyrSerGlyAspLys11eTyr 80
      240 CCAGCTGATATACAGAAAGGTGAGTCAAGTATATTTATATCTGAGACAAATTTAT 239
QY      81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
      300 GATGACTACTATCCAGATCTGAAAGGCCGAGTCACTTTACGAGTATGATCTCAATCT 359
QY      101 GlyAspAlaSer11eAsnVal1ThrAsnLeuGlnLeuSerAsp11eGlyTyrGlnCys 120
      360 GGTGATGTCATCAATTAATGTAACCAATTTCAACTGTCAGATATTTGGCACATATCACTGC 419
QY      121 LysValLysValAspProGlyValGlyAsnLysLys11eGlnLeuThrValLeuLeuLys 140
      420 AAAGTGAAGAAAGCTCTGCTGTTGCAATTAAGAGATTCATCTGTAAGTCTTGTAAAG 479
QY      141 ProSerGlyTyrArgCysTyrValAspGlySerGluGlu11eGlyAsnAspPheLysLeu 160
      480 CTTTCAGGTGCGAGATCTTACGTTGATGATGATCGAATAAATTGGAACTGACTTTAAGATA 539
QY      161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
      540 AAATGTGAACCAAAAGAGGTTCACCTTCAGATATGAGTGGCAAAATTTGCTGCAC 539
QY      181 SerGluLysLeuProThrLeuTyrPLeuAlaGluMetThrSerProVal11eSerValLys 200
      600 TCAAGAAATAGCCCACTTATGCTTACGAAATGACCTTCATCTGTTAATCTGTAA 659
QY      201 AsnAlaSerThrGluTyrSerGlyTyrThrTyrSerCysThrValLysAsnArgValGlySer 220
      660 AATGCCCTCTCTGATGCTCTGGGACATACAGCTGTACAGTCAAGAAACAGAGTGGCTCT 719
QY      221 AspGlnCysLeuLeuArgLeuAspVal1ProProSerAsnArgAlaGlyThr11eAla 240
      720 GATCAGAGCTGTTGCTGCTTAAAGCTGCTCCCTTCAATTAAGCTGAGTAATTTGCA 779
QY      241 GlyAlaVal11eGlyValLeuLeuAlaLeuValLeu11eGlyLeu11eIlePheCysCys 260
      780 GGAAGCAATTAAGGAACTTGTGCTGCTAGCGCTCATTTGATCATCTTTGCTGT 839
QY      261 Arg 261
      840 CGT 842
Db

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RESULT 2
US-08-928-383B-3
; Sequence 3, Application US/08928383B
; Patent No. 6210921
; GENERAL INFORMATION:
; APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
; APPLICANT: and Marshall S. Horwitz
; TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,383B
; FILING DATE: 12-SEP-1997
; CLASSIFICATION:
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 60/026,100
; FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ. ID NO. 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
; US-08-928-383B-3
;
; Alignment Scores:
; Pred. No.: 1,12e-142 Length: 1095
; Score: 1224.00 Matches: 232
; Percent Similarity: 93.87% Conservative: 13
; Best Local Similarity: 88.89% Mismatches: 16
; Query Match: 90.07% Indels: 0
; Gaps: 0
; DB: 4
;
; US-09-899-634c-2 (1-261) x US-08-928-383B-3 (1-1095)
;
QY      1 MetAlaLeuLeuLeuCysPheVal11eLeuCysGlyValAlaAspLeuThrArgSerLeu 20
      1 ATGGCGCTCTCTGCTGCTGCTTCCGCTCTCTGCGGAGTGGATTTCCGCAGAAATTTG 60
QY      21 Ser11eThrThrProGluGlnMet11eGluValAlaValGlyGluThrAlaTyrLeuPro 40
      61 AGTATCACTACTCTCTGAGAGAGATGATTGAAGAAAGCCAAAGGGGAAACTGCTTATCTGCCG 120
QY      41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAsp11eGluTyrPLeuLeuSer 60
      121 TGCMAATTATACGCTGATGCTCCGGAAGACCAAGGAGCCGCTGACATCGAGTGGCTGATATCA 180
QY      61 ProAlaAspAsnGlnValAspGlnVal11eLeuTyrSerGlyAspLys11eTyr 80
      181 CCAGCTGATATACAGAAAGGTGAGTCAAGTATATTTATATCTGAGACAAATTTAT 240
QY      81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
      241 GATGACTACTATCCAGATCTGAAAGGCCGAGTCACTTTACGAGTATGATCTCAATCT 300
QY      101 GlyAspAlaSer11eAsnVal1ThrAsnLeuGlnLeuSerAsp11eGlyTyrGlnCys 120
      301 GGTGATGTCATCAATTAATGTAACCAATTTCAACTGTCAGATATTTGGCACATATCACTGC 360
QY      121 LysValLysValAspProGlyValGlyAsnLysLys11eGlnLeuThrValLeuLeuLys 140
      361 AAAGTGAAGAAAGCTCTGCTGTTGCAATTAAGAGATTCATCTGTAAGTCTTGTAAAG 420
QY      141 ProSerGlyTyrArgCysTyrValAspGlySerGluGlu11eGlyAsnAspPheLysLeu 160
      421 CTTTCAGGTGCGAGATCTTACGTTGATGATCTGAAAGAAATTGGAAGTGACTTTAAGATA 480
QY      161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
      481 AAATGTGAACCAAAAGAGGTTCACCTTCATTAACAGTATGAGTGGCAAAATTTGCTGCAC 540

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| | | | |
|----|-----|---|-----|
| Qy | 181 | SergInLysLeuProThrLeuThrIleuAlaGluMetThrSerProValIleSerValLys | 200 |
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| Db | 541 | TCACGAAAAATCCCACTTCATCGTTAGCGAAGAAATACCTTCATCTGTATATCTGTAAA | 600 |
| Qy | 201 | AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer | 220 |
| | | ::: | |
| Db | 601 | AATGGCTCTTCAGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGGGGCTCT | 660 |
| Qy | 221 | AspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAla | 240 |
| | | ::: | |
| Db | 661 | GATCAGTGGCTGTGGGTCTAAACGTTGTGCCCTCTTCANAATAAAGCTGACCTAATTGCA | 720 |
| Qy | 241 | GlyAlaValAlaIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePheCysCys | 260 |
| | | ::: | |
| Db | 721 | GGAGCGCATTAATAGAACTTTGCTGTGCTCTAGCGCTCATTTGCTTATCATCTTTTGCTGT | 780 |
| Qy | 261 | Arg | 261 |
| | | | |
| Db | 781 | GCT | 783 |

```

ADDRESS: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
City: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1515 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1095
US-08-928-383B-25

Alignment Scores:
Pred. No.: 1.87e-141 Length: 1515
Score: 1216.00 Matches: 229
Percent Similarity: 93.85% Conservative: 15
Best Local Similarity: 88.08% Mismatches: 16
Query Match: 89.48% Indels: 0
DB: 4 Gaps: 0

US-09-899-634C-2 (1-261) x US-08-928-383B-25 (1-1515)
QY 1 MetAlaIeuenuenuCysPheValIeuenuCysGlyValAlaAspLeuThrArgSerIeu 20
Db 1 ATGGCGGCGCTACTGCTTGCTTCGGCTCTGTGCGGAGATCGCGGATTTCACCAAGTGTTG 60
QY 21 SerIleThrProGluIneCilIeGlyAlaIysGlyGluThrAlaTyLeuPro 40
Db 61 AGCATCATTACACCCGACAGAGATCGAAAAAGCCAAAGGGAAACCTGCTATTACCA 120
QY 41 CysArgPheThrIeuGlyProGluAspGlnGlyProLeuAspIleGluTyPLeuSer 60
Db 121 TGGCAAGTTTACTCTCAGTCCCGCAAGCCAGGACCACTGACATTGAGTGCATATCC 180
QY 61 ProAlaAspAsnGlnIysValAspGlnValIleIleuTyTserGlyAspValIleTy 80
Db 181 CCGCTGATACCAAGATAGTGAATCAAGATCATTTGTATTCGGAGAACAAATTAT 240
QY 81 AspAspTyTyTyrGlnAspLeuIysGlyArgValHisPheThrSerAsnAspLeuIysSer 100
Db 241 GATTACTACTATCCGATCTGGAAGAGACCGGATGACATTTTACAGATACGATGCTAAGCT 300
QY 101 GlyAspAlaSerIleAsnValThrAsnIeuGlnIeuSerAspIleGlyThrTyGlnCys 120
Db 301 GCGCAGCCATCTTAATATGACCAACCTGCAAGCTGTGCGACATTGGCACTTACCAAGTGC 360
QY 121 LysValIysValIaProGlyValGlyAsnIysIleGlnIeuThrValIeuLeuIys 140

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Db 361 A A A T G A A G A A A G C C C C T G G G G G T T G C A A A T A A G A A A T T C T G C T G A C C G T T C T T G T T A A G 420

Qy 141 P r o s e r g l y t h r a g c y s t y r v a l a s p g l y s e r g l u g l i l e g l y a s a s p h e l y s l e u 160

Db 421 C C T T C A G T A C A A A T G C T T G T T G A T G A T C G G A A G A G A T T G A A A T G A C T T C A A G C T A 480

Qy 161 L y s C y s g l u p o l y s g l u g l y s e r l e u p r o b e u l e u t y r g l u t r p g l n l y s e u s e r a e n 180

Db 481 A A A T G T A A C C C A A G A A G A G C T C C C T T C A C T A C A G T T G A A T G C A G A A A C T G T C G A C 540

Qy 181 S e r g l n l y s l e u p r o t h r l e u t r p l e u a l a g l u m e t h r s e r p r o v a l l e s e r v a l l y s 200

Db 541 T C C C A G A C A A T G C T T A C C C A T G C T G C A G A A A T G A C G T C A C C A G T T A T A T C T G T G A A G 600

Qy 201 A s n a l a s e r t h r g l u t y r s e r g l y t h r y s e r c y s t h r v a l l y s a s n a r y a l g l y s e r 220

Db 601 A A C C C A G T T C T G A T A T T C T G G A C A T A C A G C T G C A C G T T C A A A A C A G A C T G G G C T C T 660

Qy 221 A s p g l n c y s l e u l e u a r g l e u a s p v a l a p r o p r o s e r a s n a r a l a g l y t h r l e a l a 240

Db 661 G A C C A G T A T G C T G C G A C T A G A G T T G C C A C C T C A A C G A G C G A A C G A T C G G 720

Qy 241 G l y a l a v a l l e g l y a l l e u l e u a l a e u v a l l e u l l e g l y l e u l l e i l e p h e y c y s 260

Db 721 G G C C C C C T C A T A G G A G A C G C T G C T G C C C T T T G C T C A T C G G G C C A T C C T C T T C T G C T 780

RESULT 5

US-08-597-495B-23

Sequence 23, Application US/08597495B

Patent No. 5712369

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;

APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;

APPLICANT: Carlmel, B.; Ji, Hong; Burgess, Anthony W.;

APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron

TITLE OF INVENTION: Colon Cell And Colon Cancer Cell

TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felle & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/597,495B

FILING DATE: 02-Feb-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/511,876

FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5712369man D.

REGISTRATION NUMBER: 30,946

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 688-3884

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 960 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-597-495B-23

Alignment Scores:

Pred. No.: 3,39e-34 Length: 960
 Score: 351.50 Matches: 89
 Percent Similarity: 54.41% Conservative: 53
 Best Local Similarity: 34.10% Mismatches: 96
 Query Match: 25.86% Indels: 23
 DB: 1 Gaps: 11

US-09-899-634c-2 (1-261) x US-08-597-495B-23 (1-960)

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QY 10 LeuCyGgIyValAlaAspLeuThrArgSerLeuSerIleThrProGluGlnMetIle 29
   |||||
Db 34 CTCTGTGCAGTCAAGGTCACCGTCATCCATCTCTGTGAAACTCCGACGACGCTTCT 93
   |||||
QY 30 GluValAlaValGlyGluThralaTyrlleuProCysArgPheThrLeuGlyProGluAsp 49
   |||||
Db 94 CGGGCTTCGACGAGGAAGATGTCACCTGCGCTGCACCTACACACTTCACCTCCAGT 153
   |||||
QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspAnglnLys 66
   |||||
Db 154 CGAGAGGACTT---ATTCAATGGATTAAGCTCTCTCCTCACT-----CAT 195
   |||||
QY 67 ValAspGlnValIleIleLeuTyrlleuTyrlleuSerGlyAspLys-----IleTyrlleuAspPtyr 84
   |||||
Db 196 ACGGAAGAGGTGTCATCTGCGCTTTTCAAACTACATCCATGTCAGCTTAT 255
   |||||
QY 85 GlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSerGlyAspAlaSer 104
   |||||
Db 256 -----AAGATGCGCTCAGCATATA---TCCAAATGCTGAGCAGTCCGATGCTCC 303
   |||||
QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrGlnCysLysValLysLys 124
   |||||
Db 304 ATCACCATTGATCAGTGCACGATGACCAAGGTCGACCAAGGACCTACAGAGTCTGTGCTGCTG 363
   |||||
QY 125 AlaProGlyVal-----GlyAsnLysLys-----IleGlnLeuThrValLeuLeuLysPro 141
   |||||
Db 364 ATGTGAGACTGAGAGGCAACACCAAGTCACTGCTCGCTGTGCTCTGCGCACC 423
   |||||
QY 142 SerGlyThrArgCysTyrlleuValAspGlySerGluGlnIleGlyAsnAspPheLysLys 161
   |||||
Db 424 TCCAAACCAAGATGCGCATGACGAGAGACCATTAATGGGAACAATCCAGCTGACC 483
   |||||
QY 162 CysGluProLysGluGlnSerLeuProLeuLeuTyrlleuTrpGlnLysLeuSer---Asn 180
   |||||
Db 484 TCCCATCAAAAGAGGCTCACCAACCTCAGTACAGCTGGAAGAGGACCAATCCAGCTG 543
   |||||
QY 181 SerGlnLysLeuProThrLeuTrpLeuAlaGlnMetThrSer---ProValIleSerVal 199
   |||||
Db 544 ATTCAGGAGCAGCC-----CTGGCCCAAGCAGCTCAGCTCAGCTGCTCTCC 594
   |||||
QY 200 LysAsnAlaSerThrGluTyrlleuSerGlyThrTyrlleuSerCysThrValLysAsnArgValGly 219
   |||||
Db 595 AAGAAATATCTCCACACACATCGGTTACTACTGTAATCCCTCCAGCAATAGAGGG 654
   |||||
QY 220 SerAspGlnCysLeuLeuArgLeuAspValAlaProProSerAsnArgAlaGlyThrIle 239
   |||||
Db 655 ACGCACTTGTGCAACATCAAGGTCGCTCAGATCTCCTCCATGAGAGCTGCGCTGAT 714
   |||||
QY 240 AlaGlyValValIleGlyValLeuLeuAlaValLeuIleGlyLeuIleIlePheCys 259
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QY 260 Cys 260
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Db 775 TGC 777

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RESULT 6

US-09-068-051A-23
 ; Sequence 23, Application US/09068051A
 ; Patent No. 6291235

GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
 Simpson, Richard J.; Nice, Eduard; Moritz, R. L.;
 Catimel, B.; Ji, Hong; Burgess, Anthony W.;

Heath, Joan K.; White, Sara J.; Johnstone, Cameron
 TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
 Associated Nucleic Acid Molecules, Protein And Peptides
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fulbright & Jaworski LLP
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 360 Kb storage

COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/068,051A

FILING DATE: 10-Dec-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/597,495

FILING DATE: 02-Feb-1996

APPLICATION NUMBER: 08/511,876

FILING DATE: 04-Aug-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6291235man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5316.2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3168

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 23

SEQUENCE CHARACTERISTICS:

LENGTH: 960 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 23

US-09-068-051A-23

Alignment Scores:
 Pred. No.: 3,39e-34 Length: 960
 Score: 351.50 Matches: 89
 Percent Similarity: 54.41% Conservative: 53
 Best Local Similarity: 34.10% Mismatches: 96
 Query Match: 25.86% Indels: 23
 DB: 4 Gaps: 11

US-09-899-634c-2 (1-261) x US-09-068-051A-23 (1-960)

```

QY 10 LeuCyGgIyValAlaAspLeuThrArgSerLeuSerIleThrProGluGlnMetIle 29
   |||||
Db 34 CTCTGTGCAGTCAAGGTCACCGTCATCCATCTCTGTGAAACTCCGACGACGCTTCT 93
   |||||
QY 30 GluValAlaValGlyGluThralaTyrlleuProCysArgPheThrLeuGlyProGluAsp 49
   |||||
Db 94 CGGGCTTCGACGAGGAAGATGTCACCTGCGCTGCACCTACACACTTCACCTCCAGT 153
   |||||
QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspAnglnLys 66
   |||||
Db 154 CGAGAGGACTT---ATTCAATGGATTAAGCTCTCTCCTCACT-----CAT 195
   |||||
QY 67 ValAspGlnValIleIleLeuTyrlleuTyrlleuSerGlyAspLys-----IleTyrlleuAspPtyr 84
   |||||
Db 196 ACGGAAGAGGTGTCATCTGCGCTTTTCAAACTACATCCATGTCAGCTTAT 255
   |||||
QY 85 GlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSerGlyAspAlaSer 104
   |||||
Db 256 -----AAGATGCGCTCAGCATATA---TCCAAATGCTGAGCAGTCCGATGCTCC 303
   |||||
QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrGlnCysLysValLysLys 124
   |||||

```


RESULT 8
US-09-068-051A-31
Sequence 31, Application US/09068051A
Patent No. 6291235
GENERAL INFORMATION:
APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;
Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;
Cattmel, B.; Ji, Hong; Burgess, Anthony W.;
Heath, Joan K.; White, Sara J.; Johnstone, Cameron
TITLE OF INVENTION: Colon Cell And Colon Cancer Cell
Associated Nucleic Acid Molecules, Protein And Peptides
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068, 051A
FILING DATE: 10-Dec-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597, 495
FILING DATE: 02-Feb-1996
APPLICATION NUMBER: 08/511, 876
FILING DATE: 04-Aug-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6291235man D.
REGISTRATION NUMBER: 30, 946
REFERENCE/DOCKET NUMBER: LUD 5316.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
LENGTH: 2565 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31
US-09-068-051A-31
Alignment Scores:
Pred. No.: 1,64e-33 Length: 2565
Score: 351.50 Matches: 89
Percent Similarity: 54.41% Conservative: 53
Best Local Similarity: 34.10% Mismatches: 96
Query Match: 25.86% Indels: 23
DB: 4 Gaps: 11
US-09-899-634c-2 (1-261) x US-09-068-051A-31 (1-2565)
QY 10 LeuCyGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluGlnMetIle 29
Db 146 CTCGTGACGATCAGGAGTACCGTCGATGCATCTCTGTGAACTCCGAGGAGCTTCTT 205
QY 30 GluValAlaIleGlyGlnThrAlaIleTyrLeuProCysArgPheThrIleGluGlyProGluAsp 49
Db 206 CGGCTTCGAGGAGAAAGAGTGCACCTGCTGCACCTACACACTTCACCTCCAGT 265
QY 50 GlnGlyProLeuAspIleGluTrp-----LeuLeuSerProAlaAspGlnIlys 66
Db 266 CGAGAGGAGACTT---ATTCAATGGAGTAAGCTCTCTCTACT-----CAT 307
QY 67 ValAspGlnValIleIleIleTyrSerGlyAspIlys-----IleTyrAspAspTyrTyr 84

Db 308 ACGAAAGGGTGTCTATCTGGCCGTTTCAAAACAAAACCTACATCCATGCTGACTTAT 367
QY 85 GlnAspLeuIleGlyValArgValHisPheThrSerAsnAspLeuIleGlySerGlyAspAlaSer 104
Db 368 -----AAGATGCGCTCAGCAT---TCCACAAATGCTGAGAGTCCATGCTCTC 415
QY 105 IleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCysIleValIlys 124
Db 416 ATCACCATTGAATCAGCTGACCATGCTGCAACAGGACCTACAGAGTGTCTCTGCTG 475
QY 125 AlaProGlyVal---GlyAsnIlys-----IleGlnLeuThrValLeuLeuIysPro 141
Db 476 ATGTACAGCTTGAGGAGCAACACCAAGTACCTGCTGCTGTGCTCTGCGCACCC 535
QY 142 SerGlyThrArgCysTyrValAspIleGlySerGluGlnIleGlyAsnAspPheIleIys 161
Db 536 TCCAAACCAAGATGCGGATCCAGGAGAGACCATTAATTGGAAACAATCCAGCTGACC 595
QY 162 CysGluProIleGlyGlnIleSerLeuProLeuLeuTyrGluTrpGlnIleIysLeuSer---Asn 180
Db 596 TCCCAATCAAGAGAGGCTCACCAACCCCTCAGTACAGCTGGAAGAGTAACAATCTCTG 655
QY 181 SerGlnIleLeuProThrIleuThrIleuAlaGluMetThrSer---ProValIleSerVal 199
Db 656 AATCAGAGACAGCC-----CTGGCCAGCCAGCTCAGTACGCTGCTCTCTG 706
QY 200 IysAsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValIysAsnArgValGly 219
Db 707 AAGATATCTCCACAGACATCGGTTACTGATCTGTAACCTCCAGCAATGAGAGGGG 766
QY 220 SerAspGlnCysLeuLeuArgLeuAspValIleProPheSerAsnArgAlaGlyThrIle 239
Db 767 ACGCAGTCTGCACATCAGCGTGGCGGTGACATCTCCTCATGAAGCTGGCCCTGTAT 826
QY 240 AlaGlyAlaValIleGlyValLeuLeuAlaValLeuIleGlyLeuIleIlePheCys 259
Db 827 GTGGCATCGCGTGGCGGTGTTGACGCTCATATCATGATGATGATCATCTATCTATC 886
QY 260 Cys 260
Db 887 TGC 889
RESULT 9
US-09-336-536-68
Sequence 68, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bosson, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336, 536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 68
LENGTH: 2793
TYPE: DNA
ORGANISM: Homo sapiens
US-09-336-536-68
Alignment Scores:
Pred. No.: 1,88e-33 Length: 2793
Score: 351.50 Matches: 89
Percent Similarity: 54.41% Conservative: 53
Best Local Similarity: 34.10% Mismatches: 96
Query Match: 25.86% Indels: 23
DB: 4 Gaps: 11
US-09-899-634c-2 (1-261) x US-09-336-536-68 (1-2793)
QY 10 LeuCyGlyValAlaAspLeuThrArgSerLeuSerIleThrThrProGluGlnMetIle 29


```

Db      242 ATGAGGCAATTCTATTACTTTTCAGAGTGAGCAAGCTGTAGCCATCGGGCAATT 301
QY      85 GLASP---LeuysgIyArGValHiePheThSerAsnAspleuysSerGlyAspAla 103
Db      302 AAAGATGCAATTACAGG-----TCGAACGAT-----CAGGTAATGCA 340
QY      104 SerLeuAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyGlnCysLysValLys 123
Db      341 TCATCACTACTTCGTGCATGACAGCCAGACAGTGAATTATCATCTCGATGTTAAAC 400
QY      124 LysAlaPro-----GlyValGlyAsnLysLysIleGlnLeuThrValLeuLys 140
Db      401 AACCCCCAGACTTTCTCGGCCAAACCAAGGCACTCTCAACGTCAGCTGTGTAGTAAA 460
QY      141 ProSerGlyThrArGysTyRValAspGlySerGlnGluIleGlyLeuAsnAspPheLysLeu 160
Db      461 CTTTCTAAGCCCTTTGTAGCTTCAAGGAAAGACCAAACTGGCCACACTATTTCCCTT 520
QY      161 LysCysGluProLysGlnGlySerLeuProLeuLeuTyGlnTrpGlnLysLeuSerAsn 180
Db      521 TCCTGTCTCTGTGGCTTGGAAACCTTCCCTGTGTACTGACTGATTAACCTTGAGGA 580
QY      181 SerGlnLysLeuProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValLys 200
Db      581 AGAGACATCGTCGACGAGAAAGAAACCTCAACCCCAACCGGAGATTGGTCATTGGA 640
QY      201 AsnAlaSerThrGluTyRserGlyThrTyRserCysThrValLysAsnArgValGlySer 220
Db      641 AATTCGCAAAATTTTGAACCAAGGTTATTCAGATGTACTGCATCAACAGACTTGGCAAT 700
QY      221 AspGlnCysLeuLeuArgLeuAspValProProSerAsnArgAlaGlyThrIleAla 240
Db      701 AGTTCCTGCG-----GAATCGATCTCATCTTCCATCCAGAAAGTTGATATTGTT 754
QY      241 GlyAlaValIleGlyValLeuLeu--AlaLeuValLeuIleGlyLeuIleIlePhe 258
Db      755 GGGGCCCTTGATGTGACTGCTGTAGTGGCCGCAATCATCTCTGTGTGTGCTTC 811

```

RESULT 13

```

US-09-336-536-38
; Sequence 38, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bosson, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-336-536-38

```

Alignment Scores:

```

Pred. No.: 5,51e-21 Length: 1182
Score: 246.50 Matches: 79
Percent Similarity: 47.46% Conservative: 52
Best Local Similarity: 28.62% Mismatches: 108
Query Match: 18.14% Indels: 37
DB: 4 Gaps: 12

```

US-09-899-634c-2 (1-261) x US-09-336-536-38 (1-1182)

```

QY      3 LeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSer----- 19
Db      37 CTGGGGGTTTGTCTCGGACCTGAGTACCTCTGTGCTTCCCGAGCTCAGANGAG 96

```

```

QY      20 LeuSerIleThrThrProGlnGlnMetIleGlnLysAlaLysGlyGluThrAlaTyRLeu 39
Db      97 TTGCACGTGCCCCCGGCGCTCAAAATATGGAAGCGGTAGAGGAGAAAGAGTGTCTC 156
QY      40 ProCysArgPheThrLeuLysProGluAsp-----GlnGlyProLeu 53
Db      157 CCGGCTGTGTACACGATGGACGAGAGTGTGTCTCCACCCTCCGGAGGTGCCATC 216
QY      54 AspIleGluTrpLeuLeuSerProAlaAspAsnGlnLysValAspGlnValIleLeu 73
Db      217 CTGATC---TGTTCTTGGA---CAAGAAGGAAGAAACCAACAGGTGTGTCTTAC 270
QY      74 TyRserGlyAspLysIleTyRAspAspTyRTrpGlnAspLeuLysGlyArg-----Val 91
Db      271 ATTAATGGA-----GTCAATGACAAATAAATCACTGGAACACCCCTGTGTC 312
QY      92 HisPheThrSerAsnAspLeuLysSerGlyAspAlaSerIleAsnValThrAsnLeuGln 111
Db      313 CAC-----CTATCTCTTTCACGGAATGTGTCTCTCGCGCGGCGCACTTCAG 360
QY      112 LeuSerAspIleGlyThrTyRglnCysLysValLys-----LysAla 125
Db      361 GAGGAGACTCTGGGACTTACCGCTGTCTGTCAATGTGACAGATGATGAAGCAAAAT 420
QY      126 ProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLeuLysProSerGlyThrArg 145
Db      421 ATAGGCCACAGCATCAAAAGCATDAGAGCTCAAAAGTCTGTTCCTCCACCTCCATCC 480
QY      146 CysTyRValAspGlySerGlnGluIleGlyAsnAspPheLysLeuLysCysGluProLys 165
Db      481 TGTAGTTTACAGGGGTGTACCTATGTGGGACCAATGTGACCTGAACAGCAAGTCCCA 540
QY      166 GlnGlySerLeuProLeuLeuTyRglnTrpGlnLysLeuSerAsnSerGlnLysLeu 184
Db      541 AGAGTAACCTACTACTGCTAGTACAGTGGAGAGGCTGCCCCATCTCCAGGTCTTC 600
QY      185 -----ProThrLeuTrpLeuAlaGluMetThrSerProValIleSerValLysAla 202
Db      601 TTGGACCAAGCTTA-----GATGCTGTTCGTGATCTTTAAAGCTCACTAACTT 651
QY      203 SerThrGluTyRserGlyThrTyRserCysThrValLysAsnArgValGlySerAspGln 222
Db      652 TCCATTGCCATGTCTGAGCTATGTCTGCAAGGCTCAAAACAGATGGGCTTTGCCAAG 711
QY      223 CysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrIleAlaGlyAla 242
Db      712 TGCACGTACCTTGGACGTGATGACAGGCTCC--AAGCTGCAGTGTGCTGTGAGCA 768
QY      243 ValIleGlyValLeuLeuAlaLeuValLeuIle--GlyLeuIleIle 257
Db      769 GTTGTGGCACTTTGTTGTTGGTTGCTGATGAGTGGGCTGTGCTCTG 816

```

RESULT 14

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US-09-336-536-37
; Sequence 37, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bosson, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 1846
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-336-536-37

```

Alignment Scores:

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Pred. No.: 5,51e-21 Length: 1846
Score: 246.50 Matches: 79
Percent Similarity: 47.46% Conservative: 52
Best Local Similarity: 28.62% Mismatches: 108
Query Match: 18.14% Indels: 37
DB: 4 Gaps: 12

```

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 1,13e-20 | length: | 1846 |
| Score: | 246.50 | Matches: | 79 |
| Percent Similarity: | 47.46% | Conservative: | 52 |
| Best Local Similarity: | 28.62% | Mismatches: | 108 |
| Query Match: | 18.14% | Indels: | 37 |
| DB: | 4 | Gaps: | 12 |

US-09-899-634C-2 (1-261) x US-09-336-536-37 (1-1846)

QY 3 LeuLeuLeuCySerValLeuLeuCySGlyValAlaAspLeuThrArgSer----- 19

143 CTGGGGGTTTGTTCTCTGGGACTGAGTACCCTGTGCTGCTTCTCCAGCTCAATGAG 202

QY 20 LeuSer1LeuThrThrProGluGlnMet1LeGluValAlaGlyGluThrAlaTyLeu 39

203 TTGCACCTGGCCCCGGGCGCTCAACAATTGGAAAGCGATAGAGGGAAGAAGTGGTCTTC 262

QY 40 ProCysArgPheThrLeuGlyProGluAsp -----GlnGlyProLeu 53

263 CCGGCTGTGACACGATGGCAGGGAGGGAGTGTGGTCCACCCCCGGGAAGTGGCCATC 322

QY 54 Asp1LeGluThrPheLeuLeuSerProAlaAspAsnGlnValAspGlnVal1Leu 73

323 CTGATC---TGGTCTTTGGAA---CAAGAAGGAAGAAGAACCAACCGAGTGTGTCTTAC 376

QY 74 TyrSerGlyAspIleTyLeuAspGlyTyTyGlnAspLeuValGlyArg-----Val 91

377 ATTAAATGA-----GTCAATGACAAATTAACCTGGAAACAGCTTGCTGTC 418

QY 92 HisPheThrSerAsnAspLeuLysSerGlyAspAlaSerTleAsnValThrAsnLeuGln 111

419 CAC-----TCTATCTCTTACGGAAATGTGTCTCCCTGCGCTGGGGGCATCCAG 466

QY 112 LeuSerAsp1LeGlyThrTyGlnCysValLys-----LysAla 125

467 GAGGAGACACTGTGGACTTACCGCTGTGTGTGCATATGACAGATGATGAAGCAAAAGT 526

QY 126 ProGlyValGlyAsnLysLys1LeGlnLeuThrValLeuLeuLysProSerGlyThrArg 145

527 ATAGGCCACGACATCAAAAGCATAGAGCTCAAGGTCTGTCTCCAGCTCCCATCC 586

QY 146 CysEtyrValAspGlySerGluGlu1LeGlyAsnAspPheLysLeuLysCysGluProLys 165

587 TGTAGTTTAAGGGGTGTACCTTATGTCCGGACCAATGTGACCTGTAACTGCATGCCCA 646

QY 166 GluGlySerLeuProLeuLeuTyrgLutrgLyn1LeuSerAsnSerGlnLysLeu--- 184

647 AGGAGTAAACCTACTGCTCAGTACCAAGTGGAGAGGCTGGCCCATCTCCACAGTCTTC 706

QY 185 -----ProThrLeuThrPheAlaGluMetThrSerProVal1LeSerValLysAsnAla 202

707 TTGGACACACCTTA-----GATGCTGTTCGTGATCTTTAAACCTCACTAACTT 757

QY 203 SerThrGluLysSerGlyThyTySerCysThrValLysAsnArgValGlySerAspGln 222

758 TCCATTGGCCATGTCTGAGCTATGTCTGTCCAGAGCTCAAAACAGTGGCTTTGGCCAG 817

QY 223 CysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrTleAlaGlyAla 242

818 TGCAACTGTGACTTTGACGTGATGAACAGGGTCC---AAGGCTGACGTGGTGTGGAGCA 874

QY 243 Val1LeGlyValLeuLeuAlaLeuValLeu1Leu---GlyLeu1Leu 257

875 GTTGTGGGCACTTTTGTGGGTGGGTGGATGACTGGGGCTGGTCTG 922

RESULT 15
US-08-979-424-2

```

; GENERAL INFORMATION:
;
; APPLICANT: Lal, Preeti
;
; APPLICANT: Corley, Neil C.
;
; TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
;

```

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,424
FILING DATE: Filed Herewith

INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:

LENGTH: 1387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGFET03
CLONE: 1232054

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 3,34e-17 | Length: | 1387 |
| Score: | 27.00 | Matches: | 70 |
| Percent Similarity: | 41.99% | Conservative: | 48 |
| Best Local Similarity: | 25.91% | Mismatches: | 113 |
| Query Match: | 15.97% | Indels: | 50 |
| DB: | 2 | Gaps: | 11 |

US-09-899-634C-2 (1-261) X US-08-979-424-2 (1-1387)

| | | | | |
|----|-----|--|--------|-----|
| Qy | 1 | LeuLeuLeuCyPheValLeuLeuLeuYsgIValAlaAspLeuThrArgSer--- | LeuSer | 21 |
| Db | 161 | CTCGGGTTTGTTCCTCGGGCGTGAAGCCCTTCGGCCCCCTCGCGAGCCCACTTCA | | 220 |
| Qy | 22 | lIeThrThrProGlUGlMetIleGlulysAlaYsgIgluThrAlaYrLeuProCys | | 41 |
| Db | 221 | CTGCACCTTGCCCGCCCAACCGGTTCGACAGCGGTGAAGGAGGAGGAAGTGTTC | | 280 |
| Qy | 42 | ArgPheThrLeuGlyProGlu-----AspGlnGlyProLeuAspIleGlu----- | | 56 |
| Db | 281 | TGGTACACCTTGACGCGGAGGTGTCTTATCCAGCCATGGAGTGGAGTCCCTTGTGATG | | 340 |
| Qy | 57 | TrpLeuLeuSerProAlaAspAsnGlnYsgIValAspGlnValIleIleLeuYrSerGly | | 76 |
| Db | 341 | TGCTTCTTCAAA-----CAGAAAGAAAGGAGGATCAGGTGTTCCTCATCAATGCGG | | 394 |
| Qy | 77 | -----AspIlyIleIyTrAspAspYrYrYrGlnAspLeuLys | | 88 |
| Db | 395 | GTCACAACAAGCAAACTGGAGTATCCTTGGCTTAC----- | | 430 |
| Qy | 89 | GlyArgValHisPheThrSerAsnAspLeuYsgIyAspAlaSerIleAsnValThr | | 108 |
| Db | 431 | -----TCCATGGCTCTCCGGAACCTGTGCTCCCTTCGCGGTGAG | | 466 |

```
QY 109 AsnLeuGlnLeuSerAsp11eGlyThrTyGlnCysIysVallys----- 123
Db 467 GGTCTCCAGGAGAAAGACTGGGCCCTACGAGCTGCCGATGTGCAAGCAACAA 526
QY 124 ---LysAlaProGlyValGlyAsnIysLysIleGlnLeuThrValLeuLeuLysProSer 142
Db 527 GGCAAATCTAGGGCCACAGCATCAAAACCTTAGACTCAATGTACTGTCTCCAGCT 586
QY 143 GlyThrArgCysTyRValAspGlySerGluGluIleGlyAsnAspPheLysLeuLysCys 162
Db 587 CCTCATCCCTCGCGCTCTCCAGGGGTGTGCCCATGTGGGGCAACGTGACCTGAGCTGC 646
QY 163 GluProLysGluGlySerLeuProLeuLeuTyGluTrpGlnLysLeuSerAsnSerGln 182
Db 647 CAGTCTCAAGAGTAAGCCCGCTGTCCAATACCACTGAGTGGATCGG----- 691
QY 183 LysLeuProThrLeuTrp-----LeuAlaGluMetThrSerProValIle 197
Db 692 CAGCTTCATCTCTCCAGACTTCTTTGCACACAGCATTTAGATGTCAATCCGTGGGCTTTTA 751
QY 198 SerValIysAsnAlaSerThrGluTySerGlyThrTySerCysThrValIysAsnArg 217
Db 752 AGCCTACCAACCTTTGTCTTCATGAGCTGAGACTATGTCTGCAAGGCCCAATGAG 811
QY 218 ValGlySerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGly 237
Db 812 GTGGGCACTGCCCAATGTAATGTGACCGTGAA---GTGAGACACAGGGCTGAGAGTGCA 868
QY 238 ThrIleAlaGlyAlaValIleGlyValLeuLeuAlaLeu---ValLeuIleGlyLeuIle 256
Db 869 GTGGTCTGAGAGCTGTGTGGGTACCTGTGTGACTGGGGTGTGGCTGGGGCTGTC 928
QY 257 Ile 257
Db 929 CTC 931
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Search completed: July 12, 2003, 13:00:48
Job time : 53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 12:41:12 ; Search time 138 Seconds
(without alignments)
2986.361 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359
Sequence: 1 MALLLCFVLGCVADLTRSL.....AVIGVLLALVLIIGLIIFCCR 261

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1105431 seqs, 789497651 residues

Total number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published Applications NA -QFMT=fastcat -SURF1=mrpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -STAR1=1 -END=-1 -MATRIX=bl0sum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcpt -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plco -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09899634 @CGN 1.1.125 @runat_09072003_111142_16473
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-LONGLOG -DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FAPOP=6 -FAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

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6: /cgnt2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
7: /cgnt2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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9: /cgnt2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgnt2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgnt2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgnt2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgnt2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgnt2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 1353 | 99.6 | 1098 | 10 | US-09-899-634A-3 |
| 3 | 1238 | 91.1 | 2434 | 10 | US-09-971-736-1 |
| 4 | 1238 | 91.1 | 2473 | 9 | US-10-176-847-77 |

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| 5 | 1238 | 91.1 | 3060 | 9 | US-09-992-598-504 | Sequence 504, App |
| 6 | 1238 | 91.1 | 3060 | 9 | US-09-989-293A-504 | Sequence 504, App |
| 7 | 1238 | 91.1 | 3060 | 9 | US-09-989-735-504 | Sequence 504, App |
| 8 | 1238 | 91.1 | 3060 | 9 | US-09-990-444-504 | Sequence 504, App |
| 9 | 1238 | 91.1 | 3060 | 9 | US-10-053-107-9 | Sequence 9, Appli |
| 10 | 1238 | 91.1 | 3060 | 9 | US-09-989-730-504 | Sequence 504, App |
| 11 | 1238 | 91.1 | 3060 | 9 | US-09-990-438-504 | Sequence 504, App |
| 12 | 1238 | 91.1 | 3060 | 9 | US-09-991-181-504 | Sequence 504, App |
| 13 | 1238 | 91.1 | 3060 | 9 | US-09-993-687-504 | Sequence 504, App |
| 14 | 1238 | 91.1 | 3060 | 9 | US-09-989-734-504 | Sequence 504, App |
| 15 | 1238 | 91.1 | 3060 | 9 | US-09-997-653-504 | Sequence 504, App |
| 16 | 1238 | 91.1 | 3060 | 9 | US-09-993-687-504 | Sequence 504, App |
| 17 | 1238 | 91.1 | 3060 | 9 | US-09-990-438-504 | Sequence 504, App |
| 18 | 1238 | 91.1 | 3060 | 9 | US-09-990-562-504 | Sequence 504, App |
| 19 | 1238 | 91.1 | 3060 | 9 | US-09-997-428-504 | Sequence 504, App |
| 20 | 1238 | 91.1 | 3060 | 9 | US-09-997-666-504 | Sequence 504, App |
| 21 | 1238 | 91.1 | 3060 | 9 | US-10-227-884-215 | Sequence 504, App |
| 22 | 1238 | 91.1 | 3060 | 9 | US-09-990-711-504 | Sequence 215, App |
| 23 | 1238 | 91.1 | 3060 | 9 | US-10-230-163-215 | Sequence 215, App |
| 24 | 1238 | 91.1 | 3060 | 9 | US-09-989-726-504 | Sequence 504, App |
| 25 | 1238 | 91.1 | 3060 | 9 | US-09-989-726-504 | Sequence 504, App |
| 26 | 1238 | 91.1 | 3060 | 9 | US-09-998-156-504 | Sequence 504, App |
| 27 | 1238 | 91.1 | 3060 | 9 | US-10-218-631-215 | Sequence 215, App |
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| 36 | 1238 | 91.1 | 3060 | 9 | US-09-990-726-504 | Sequence 504, App |
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| 38 | 1238 | 91.1 | 3060 | 9 | US-09-997-601-504 | Sequence 504, App |
| 39 | 1238 | 91.1 | 3060 | 9 | US-09-989-728A-504 | Sequence 504, App |
| 40 | 1238 | 91.1 | 3060 | 9 | US-09-990-440-504 | Sequence 504, App |
| 41 | 1238 | 91.1 | 3060 | 9 | US-09-991-854-504 | Sequence 504, App |
| 42 | 1238 | 91.1 | 3060 | 9 | US-09-997-349-504 | Sequence 504, App |
| 43 | 1238 | 91.1 | 3060 | 9 | US-09-997-440-504 | Sequence 504, App |
| 44 | 1238 | 91.1 | 3060 | 9 | US-09-997-628-504 | Sequence 504, App |
| 45 | 1238 | 91.1 | 3060 | 9 | US-09-997-689-504 | Sequence 504, App |
| | | | | | US-10-213-145-9 | Sequence 9, Appli |

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09899634A
; Patent No. US20020059654/1
; GENERAL INFORMATION:
; APPLICANT: Thomas Buehler, Reto Andreas Gadiant, Reinhard Korn, Rao Movva
; TITLE OF INVENTION: PCR and its uses
; FILE REFERENCE: 4-31499A
; CURRENT APPLICATION NUMBER: US/09/899,634A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: porcine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3229)..(4014)
US-09-899-634A-1

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| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

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| / | GENERAL INFORMATION: | | |
| / | APPLICANT: No. US20020132769Aiatris AG | | |
| / | TITLE OF INVENTION: Targeting molecules | | |
| / | FILE REFERENCE: 4-31615/GII | | |
| / | CURRENT APPLICATION NUMBER: US/09/971,798 | | |
| / | CURRENT FILING DATE: 2001-10-05 | | |
| / | NUMBER OF SEQ ID NOS: 31 | | |
| / | SOFTWARE: PatentIn version 3.1. | | |
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| / | LENGTH: 2434 | | |
| / | . TYPE: DNA | | |
| / | ORGANISM: Homo sapiens | | |
| / | FEATURE: | | |
| / | NAME/KEY: CDS | | |
| / | LOCATION: (60)..(1157) | | |
| / | OTHER INFORMATION: | | |
| / | US-09-971-798-1 | | |
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| Qy | 21 | SerIleThrThrProGIuInMeIllegIuYsaIalysGIuThraIeTyLeuPro | 40 |
| Dn | 120 | AGATCACTACTCTGAAGAGATGATTGAAAAGCAAAGGGGAACTGCCTATCTCCG | 179 |
| Qy | 41 | CysArgPheThrLeuGlYProGIusApGIuNGlYProLeuAspIllegIuTrpLeuLeuSer | 60 |
| Dn | 180 | TGC AAA TTTAACGCTTAGTCCCAAGACCAAGGACC GCTGGACATCGACTGCTGATATCA | 239 |
| Qy | 61 | ProAlAspAsnGIuNlySValAspGIuValIleIleLeuTYrSerGIYAspLysIleTyR | 80 |
| Dn | 240 | CCAGCTCATATCAGAAAGGTGATCAAGTATTATTATTATTCGAGACAATAATTAT | 299 |
| Qy | 81 | AspAspTYrTYrGIuAspLeuUysGIYArqValHisPheThrSerAsnAspLeuLysSer | 100 |
| Dn | 300 | GATGACTACTCATCAATCTGAATCGAAGGCCAGTACATTTTA CGAGTAATGATCTCAATCT | 359 |
| Qy | 101 | GIYAspAlaSerIleAsnValThrAsnLeuGIuLeuSerAspIllegIYThTYrGIuCys | 120 |
| Dn | 360 | GGTGATGCATCAATTAATGTAACTGAATTTACAACTGCATGATTTGGCACATATCACTGC | 419 |
| Qy | 121 | LysValLysLysValaProGIYValaGIYAsnLysLysIllegIuLeuThrValLeuLeuLys | 140 |
| Dn | 420 | AAAGTGA AAAAGCTCTGCTGTGTGC AAATTAAGGAATTCATCTGGTAGTCTTGTTAAG | 479 |
| Qy | 141 | ProSerGIYThzYrGYcSYrValaAspGIYSerGIuGIuIllegIYAsnAspPheLysLeu | 160 |
| Dn | 480 | CTTTCAAGTCCGAGATCTTACGTATGATGATCTGAAGAAATTTGAAGACCTTTAAGATA | 539 |
| Qy | 161 | LysCYcGIuProLYsgIuGIYserLeuProLeuLeuTYrGIuTrpGIuLysLeuSerAsn | 180 |
| Dn | 540 | AAATGTGAACCAAAAGAGTTCACTTCATTAACGTAATGATGGCAAAATTTGCTGAC | 599 |
| Qy | 181 | SerGIuNlySLeuProThrLeuTrpLeuAlaGIuMettThrSerProValIleSerValLys | 200 |
| Dn | 600 | TCCAGAAAATGCCCACTTCATGTTTAGCAGAAATGACTCATCTGTAATTCGTAAAA | 659 |
| Qy | 201 | AsnAlaSerThfGIuTYrSerGIYThTYrTYrSerCYcThNValLYsAsnArVaIGIYSer | 220 |
| Dn | 660 | AATGCTCTTCTGAGTACTCTGGAGCATTCACCTGATACATGCAGAAACAGTGGGCTCT | 719 |
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; Sequence 77, Application US/10176847
; Publication No. US2003006836A1
; GENERAL INFORMATION:
; APPLICANT: Veibiy, Peltier Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/10/176,847
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 2473
; TYPE: DNA
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; US-10-176-847-77

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| DB: | | 9 | | |
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| DB | 94 | ATGACCCTCTGTGCTTCGTTCGTCTCTGTCGAGTAGAGATTTCGCCAGAGTTTG | 15 | |
| QY | 21 | SeiLeThrThrProGluMetIleGluValAlaValSgiValuThrAlaThrLeuPro | 40 | |
| DB | 154 | AGATACATCACTCTGAAAGAGTAGTATGAAAAGCCAAAGGGAAACGCTATCTGCCA | 21 | |
| QY | 41 | CysArgPheThrLeuGluYProGluAspGlnGlyProLeuAspIleGluThrLeuLeuSer | 60 | |
| DB | 214 | TGCAAATTTACCGTTAGTCCCAACACCGAGCCGCTGGACATGACGTGCTCATATCA | 27 | |
| QY | 61 | ProAlaAspAsnGlnLeuValAspGlnValIleIleLeuYrSerGlyAspLeuSileThr | 80 | |
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| QY | 81 | AspAspTyrtTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer | 100 | |
| DB | 334 | GATGACTACTATCCAGATCTGAAGAGCCGAGTACATTTTACAGATTAATGATCTCAAACTC | 39 | |
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| DB | 394 | GGGATGACATCAATTAATATTAACGAATTTACACAGCTGACAGATATGGACATATCAGGC | 45 | |
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| 2 | PRIOR FILING DATE: 1998-06-17 |
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| 4 | PRIOR FILING DATE: 1998-06-17 |
| 5 | PRIOR APPLICATION NUMBER: 60/089601 |
| 6 | PRIOR FILING DATE: 1998-06-18 |
| 7 | PRIOR APPLICATION NUMBER: 60/089907 |
| 8 | PRIOR FILING DATE: 1998-06-18 |
| 9 | PRIOR APPLICATION NUMBER: 60/089908 |
| 10 | PRIOR FILING DATE: 1998-06-18 |
| 11 | PRIOR APPLICATION NUMBER: 60/089947 |
| 12 | PRIOR FILING DATE: 1998-06-19 |
| 13 | PRIOR APPLICATION NUMBER: 60/089948 |
| 14 | PRIOR FILING DATE: 1998-06-19 |
| 15 | PRIOR APPLICATION NUMBER: 60/089952 |
| 16 | PRIOR FILING DATE: 1998-06-19 |
| 17 | PRIOR APPLICATION NUMBER: 60/090246 |
| 18 | PRIOR FILING DATE: 1998-06-22 |
| 19 | PRIOR APPLICATION NUMBER: 60/090252 |
| 20 | PRIOR FILING DATE: 1998-06-22 |
| 21 | PRIOR APPLICATION NUMBER: 60/090254 |
| 22 | PRIOR FILING DATE: 1998-06-22 |
| 23 | PRIOR APPLICATION NUMBER: 60/090349 |
| 24 | PRIOR FILING DATE: 1998-06-23 |
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| 26 | PRIOR FILING DATE: 1998-06-23 |
| 27 | PRIOR APPLICATION NUMBER: 60/090429 |
| 28 | PRIOR FILING DATE: 1998-06-24 |
| 29 | PRIOR APPLICATION NUMBER: 60/090431 |
| 30 | PRIOR FILING DATE: 1998-06-24 |
| 31 | PRIOR APPLICATION NUMBER: 60/090435 |
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| 35 | PRIOR APPLICATION NUMBER: 60/090445 |
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| 37 | PRIOR APPLICATION NUMBER: 60/090472 |
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| 63 | PRIOR APPLICATION NUMBER: 60/091478 |
| 64 | PRIOR FILING DATE: 1998-07-02 |
| 65 | PRIOR APPLICATION NUMBER: 60/091544 |
| 66 | PRIOR FILING DATE: 1998-07-01 |
| 67 | PRIOR APPLICATION NUMBER: 60/091519 |
| 68 | PRIOR FILING DATE: 1998-07-02 |
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| 70 | PRIOR FILING DATE: 1998-07-02 |
| 71 | PRIOR APPLICATION NUMBER: 60/091633 |

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RESULT 6
US-09-989-293A-504
Sequence 504, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Feng, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090349

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR APPLICATION NUMBER: 2001-11-19
PRIOR FILING DATE: 1997-06-16
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US-09-899-634C-2 (1-261) x US-09-989-735-504 (1-3060)

RESULT 8
US-09-99

GENERAL INFORMATION:

1 APPLICANT: Ashkenazi, Avi J.
 2 APPLICANT: Baker, Kevin P.
 3 APPLICANT: Botstein, David
 4 APPLICANT: Deansyere, Luc
 5 APPLICANT: Eaton, Dan L.
 6 APPLICANT: Ferrara, Napoleone
 7 APPLICANT: Fong, Sherman
 8 APPLICANT: Gerber, Hanspeter
 9 APPLICANT: Gerritsen, Mary E.
 10 APPLICANT: Goddard, Audrey
 11 APPLICANT: Godowski, Paul J.
 12 APPLICANT: Grimaldi, J. Christopher
 13 APPLICANT: Gurney, Austin L.
 14 APPLICANT: Kijavini, Ivar J.
 15 APPLICANT: Napier, Mary A.
 16 APPLICANT: Pan, James
 17 APPLICANT: Paoni, Nicholas F.
 18 APPLICANT: Roy, Margaret Ann
 19 APPLICANT: Stewart, Timothy A.
 20 APPLICANT: Tumas, Daniel
 21 APPLICANT: Watanabe, Colin K.
 22 APPLICANT: Williams, P. Mickey
 23 APPLICANT: Wood, William I.
 24 APPLICANT: Zhang, Zemin
 25 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 26 FILE REFERENCE: P2730P1C19
 27 CURRENT APPLICATION NUMBER: US/09/990,444
 28 CURRENT FILING DATE: 2001-11-14
 29 PRIOR APPLICATION NUMBER: 60/049787
 30 PRIOR FILING DATE: 1997-06-16
 31 PRIOR APPLICATION NUMBER: 60/062250
 32 PRIOR FILING DATE: 1997-10-17
 33 PRIOR APPLICATION NUMBER: 60/065186
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 35 PRIOR APPLICATION NUMBER: 60/065311
 36 PRIOR FILING DATE: 1997-11-13
 37 PRIOR APPLICATION NUMBER: 60/066770
 38 PRIOR FILING DATE: 1997-11-24
 39 PRIOR APPLICATION NUMBER: 60/075945

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PRIOR FILING DATE: 1998-07-09

Alignment Scores:

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| Pred. No.: | 9,76e-156 | Length: | 3060 |
| Score: | 1238.00 | Matches: | 233 |
| Percent Similarity: | 94.25% | Conservative: | 13 |
| Best Local Similarity: | 89.27% | Mismatches: | 15 |
| Query Match: | 91.10% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-899-634c-2 (1-261) x US-09-989-730-504 (1-3060)

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Db 77 ATGGCGCTCTCTGCTGCTTCGTCCTCGCGGAGTAGGATTTCGCCAGAACTTGG 136
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QY 21 SerIleThThProGluInMetIleGluysAlaIysGlyGluThraIaTyrlleuPro 40
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Db 137 AGTATCATTCTCTCGAAGATGATTGAAAAGCCAAAGGGAACCTCCATTCTGCCA 196
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QY 41 CysArgPheThrIeuGlyProGluAspGingIlyProIeuAspIleGluTrpIeuIeuSer 60
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Db 197 TCGAATTTACGCTTACTCCGAGACAGGACCGCTGACATCGATGCTGATATCA 256
Qy 61 ProAlaSpaanglnlyValaspGlnValIlelleuTySerGlyAspLysIleTy 80
Db 257 CCAGCTCATATACGAAGGTGATCAAGTATTTATTTATTTCTGAGACAAAATTTAT 316
Qy 81 AspAspTyTrTglnaPleuLygIyArGValHisPheThrSerAsnApeLysSer 100
Db 317 GATGACTACTATCCAGATCTGAAGGCCGAGTCAATTTTCGAGTATGATCTCAATCT 376
Qy 101 GLYAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyGlnCys 120
Db 377 GGTGATGATCAATTAATGTAACCAATTACAATGCAATATTTGGCAATATCAATGTC 436
Qy 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLleuLys 140
Db 437 AAAGTGAANAAGCTCTGCTGTTGCANAATGAAATTCATCTGTAAGTTCTTTAG 496
Qy 141 ProSerGlyThrArGcTyTyValaspGlySerGlnGlnIleGlyAsnApePheLysLeu 160
Db 497 CTTTCAGTGGAGATGTTACGTTGATGATCTGAACAAATTTGAAGTGAAGTGAAGATA 556
Qy 161 LysCyGlnProLysGlnGlySerLeuProLeuLeuTyGlnIleLysLeuSerAsn 180
Db 557 AAATGTGAACCAAGAGGTTCACTTCATTCAGATGAGTGGCAAAATTTGCTGAC 616
Qy 181 SerGlnLysLeuProThrLeuThrLeuAlaGlnuThrSerProValIleSerValLys 200
Db 617 TCACGAAATATGCCCATCTTCATGTTGCAAAATGCAATTCATCTGTAATCTGTAATA 676
Qy 201 AsnAlaSerThrGlnTySerGlyThrTySerCyThrValLysAsnArGValGlySer 220
Db 677 AATGCTCTCTGAGTACTCTGGGACATACAGCTGATCAGTCAGAACAGAGTGGCTCT 726
Qy 221 AspGlnCysLeuLeuAlaGlnLeuAspValValProProSerAsnArGAlaGlyThrIleAla 240
Db 737 GATCAGAGCTGTTGCTGCTAAACGTTGCTCCCTCCCAATTAAGCTGCAATTAATGCA 796
Qy 241 GLYAlaValIleGlyValLleuLeuAlaLeuValLleuIleGlyLeuIleIlePheCysCys 260
Db 797 GAGGCCATTAAGGAATTTGCTTCTGCTTACGCTCATTTGGCTTATCATCTTTGCTGT 856
Qy 261 Arg 261
Db 857 CGT 859

RESULT 11
US-09-990-436-504
Sequence 504, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 9,76e-156 Length: 3060
Score: 1238.00 Matches: 233
Percent Similarity: 94.25% Conservative: 13
Best Local Similarity: 89.27% Mismatches: 15
Query Match: 91.10% Indels: 0
DB: 9 Gaps: 0
US-09-899-634c-2 (1-261) x US-09-990-436-504 (1-3060)

QY 1 MetAlaLeuLeuLeuCySpheValLeuLeuCyGlyValAlaAspLeuThrArgSerLeu 20
DB 77 ATGGGCGCTCTCGTGGCTTCCGTCTCCGTGCGGAGTAGTGATTCGCCAGAGTTGG 136
QY 21 SerIleThrProGluGlnMetIleGluValAlaValGluThrAlaTyrLeuPro 40
DB 137 AGTATCTACTCTCGAGAGATGATGAAAGCCAAAGGGGAAATGCTTATCTGCCA 196
QY 41 CyArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTyrPheLeuSer 60
DB 197 TCGCAATTATACGCTTAGTCCGAGACGAGCCGCTGAGATCGAGTGGCATATCA 256
QY 61 ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
DB 257 CCAGCTGATTAATCAGAGGTGATCAAGTATTTATTTATTCGAGACAAATTAT 316
QY 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
DB 317 GATGACTTATCTCAGATCTGAAGCCGAGTACATTTCAGATATGATCTCAATCT 376
QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
DB 377 GGTGATGATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 436
QY 121 LysValLysValAlaProGlyValGlyValLysValLysValLysValLysValLysVal 140
DB 437 AAAGTCAAAAAGCTCTCGTGTTCGCAATAAGAAATTCATCTGAGTCTTGTAA 496
QY 141 ProSerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
DB 497 CCTCAGGTGCGAGATGTTACGTTGATGATCGAAGAAATTCATTAAGATA 556

Qy 161 LysCysGluProlysglySerleuProleuLeuTyrglyTrpGlnlySleuSerAsn 180
Db 557 AAATGTAAACCAAAAGAGGTTCATTCATTAAGATGAGGCAAAATGCTGAC 616
Qy 181 SerGlnlyLeuProlyTrpLeuTrpLeuAlaGlnMetThrSerProValIleSerValys 200
Db 617 TCAAGAAATGACCCACTTCAATGATTGACAGAAATGACTTCACTTATATCTGTAATA 676
Qy 201 AsnAlaSerThrGlnlyTrpSerGlyThrTySerCysThrValIlyAsnArgValGlySer 220
Db 677 AATGCCCTTCTGAGTACTCTGGGACATACAGCTGTCAGTCAAGAAACAGAGGGGCTCT 736
Qy 221 AspGlnCysleuLeuAlaGlyLeuAspValValProProSerAsnArgAlaGlyThrIleAla 240
Db 737 GATCAGAGCCTGTTGCTGCTTAAACGTTGCTCCCTTCAATAAAGCTGAGCTAATTGCA 796
Qy 241 G1yAlaValIleGlyValIleLeuLeuAlaLeuValleuIleGlyLeuIleIlepeCysCys 260
Db 797 GGAGCCATTATAGGAACCTTGTGCTGCTTACGCCCTCATGCTTATCATCTTTGCTGT 856
Qy 261 Arg 261
Db 857 CGT 859
RESULT 12
US-09-991-181-504
Sequence 504, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-17

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| | : | PRIOR FILING DATE: 1998-07-02 | : |
| | : | PRIOR APPLICATION NUMBER: 60/091978 | : |
| | : | PRIOR FILING DATE: 1998-07-07 | : |
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| | : | PRIOR FILING DATE: 1998-07-09 | : |
| | | | |
| Alignment Scores: | | | |
| Pred. No.: | | 9,76e-156 | Length: 3060 |
| Score: | | 1238,00 | Matches: 233 |
| Percent Similarity: | | 94,25% | Conservative: 13 |
| Best Local Similarity: | | 89,27% | Mismatches: 15 |
| Query Match: | | 91,10% | Indels: 0 |
| DB: | | 9 | Gaps: 0 |
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| US-09-899-634C-2 (1-261) x US-09-991-181-504 (1-3060) | | | |
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| Dd | 77 | ATGGCCCTCGTGTGCTTCGTGCCTCGTGCGAGTAGTGATTGCCAGAAGTTTG | 136 |
| OY | 21 | Se1LeThThProglInMe1IegluysalatsglsyIuthra1atyLeuPro | 40 |
| Dd | 137 | AGTAACACTACTCTGAAGAGATGATGAAAGCCAAGGGAAGAACTGCTATCTCCA | 196 |
| OY | 41 | CysArSPhethrLeuglyProgluaSpnglYProleaApplIeglutRpleuLeuSer | 60 |
| Dd | 197 | TGGAATTTACGCTTAGTCCGAAACACAGGACCCTCGACATCGAGTGGCTGATATCA | 256 |
| OY | 61 | ProAlaaspAnslInlyValaspglnVallelleutyrsErglyAspLysIlEtYr | 80 |
| Dd | 257 | CCAGCTCATATACAGAAAGTCGATCAAGTGAATTATTATTTCTGAGACAAAATTTAT | 316 |
| OY | 81 | AspaSPDYTYcInlaSpneuLyScglVarygVAHIsPhethrSaanaapLeuLySer | 100 |
| Dd | 317 | GATGACTACTATCCACAATCTGGAAGCCGAGACTTTTACAGATAATGATCTCAATCT | 376 |
| OY | 101 | GlYAsPa1aser1IeaSnValThrAsnleugInleuSeRaPlIeglyThryGrInCyS | 120 |
| Dd | 377 | GGTGAATCATCAATTAATTAATTAAGAAATTTACAACCTGATGATTTGGCACATATCAAGTC | 436 |
| OY | 121 | LyeValLysLysLaBProglYvalGlYasnLysylIegInleuthrValleuLeuLys | 140 |
| Dd | 437 | AAAGTGA AAAAGCTCTCGTGTGCAATAA GAAGATTCACTGTGATGTTCTTGTAAG | 496 |
| OY | 141 | ProSerGlyThrArgCyStyryValaspglySerGluIleglyAsnaSpheLysLeu | 160 |
| Dd | 497 | CTTCAGGGTCCGAGATGACCTTATGATGATCGAAGAAATTTGAAGACTTTTAAATA | 556 |
| OY | 161 | LysCySGlUpProlyagInglYserLeuProlenLeuTyrgIUTrPGLNLYseuSerSn | 180 |
| Dd | 557 | AAATGTGAACCAAAAGAGGTTCACTTCATTACGATGATGAGTGGCAAAAATTTGTCTGAC | 616 |
| OY | 181 | SerGlnLysLeuProThreutrPleuAaglunetrPserProValIIeserVallys | 200 |
| Dd | 617 | TCAAGAAATGCCCACTTCATGGTTAGAGAAATGACTTCATCGTTATATCTGTAAA | 676 |
| OY | 201 | Asna1aserThrcIuTyrsErglyThryrsCyStrValLySasnaRva1GlySer | 220 |
| Dd | 677 | AATGCTCTTCTTGAGTACTCTGGGACATACAGCTGTATACGACAAAA CAGAGTGGCTCT | 736 |
| OY | 221 | AspGlnCyBeuLeuArgLeuaspyValAProPserSaanaAg1aGlyThrlala | 240 |
| Dd | 737 | GATCAGGCTGTGGGTCAAACGTGTGCTCTTCAAAATTAAGCTGACCTAATTGCA | 796 |
| OY | 241 | GlYAlaAvalIeglyValleuLeuA1aenValleuIleglyLeuIlellepheCyCys | 260 |
| Dd | 797 | GGAGCCATTATAGAACCTTTGCTTCTCTAGGCGCTCATGGTCTTATCATCTTTTGGCTGT | 856 |
| OY | 261 | Arg 261 | |
| Dd | 857 | CGT 859 | |

RESULT 13
US-09-993-687-504
Sequence 504, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993.687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349

Oy 1 MetAlaleuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerIeu 20
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|||
Dd 77 ATGGCGTCTCCTGCTGTGCTTCGTGCTCCGTGGAGATGATGATTTCGCCAAGAAATTG 136
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|||||
Oy 21 SerIleuThrProGluGlnMetIleGluPsaIalPsaGlyGluThrAlaTyrlendro 40
|||
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|||

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Db      137 AGTACCACTACTCCCTCGAAGAGATGATTTGAAAAGCCAAAGGGGAACCTGCTATCTGCCA 196
QY      41  CysaTgPheThrLeuGlyProGlnAspGlnGlyProLeuAspIleGluTrpLeuLeuSer 60
Db      197 TGCAAATTTACGCTTAGTCCCGAAGACCCGAGGACCGCTGGAATCATCAGTGGCTGATATCA 256
QY      61  ProIlaaPaenGlnIleValAspGlnValIleIleLeuTySerGlyAspIleIleTyR 80
Db      257 CCAGCTGATTAATCAGAAGGTGATCAAGATTAATTTATTTATTTATTTCTGGAGACAAATTTAT 316
QY      81  AspaEPlyTYRGINAspLeuIysGlyIArgValIhIspheThrSerAsnAspLeuIysSer 100
Db      317 GATGACTACTCTCCAGATCTGAAAGCCGAGTACATTTTACGAGTATATGATCTCAATCT 376
QY      101 GlnAspaIaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyGlnCys 120
Db      377 GGTATGATCATCAATTAATGTATACGAATTTACAACGTGCAGATATTGGCACAATTCAGTGC 436
QY      121 LysValIleValIleProGlyValIleGlnAsnIleValIleGlnLeuThrValLeuLeuIys 140
Db      437 AAAGGAAAAAAGCTCTCGTGTTCCAATAAGAAAGATTCATCTGGTACGTTCTTGTTAG 496
QY      141 ProSerGlyThrArgCysTyrValAspGlySerGlnIleIleGlyAsnAspPheIysLeu 160
Db      497 CTTTAGGTCGAGATGTTACCTTATGATGATCTGAAAGAAATTGGAAGTGACTTTAAGATA 556
QY      161 LysCysGlnProIysGlnGlySerLeuProLeuLeuTyGluTrpGlnIysLeuSerAsn 180
Db      557 AAATGTGAACCAAAAGAAAGTTCACCTTCATTCACGATAGAGAGCGCAAAAATTTGTGTGAC 616
QY      181 SerGlnIysLeuProThrLeuTrpLeuIleGluMetThrSerProValIleSerValIys 200
Db      617 TCACAGAAAAAGCCCACTTCATGATGTTAGCAGAAAGCACTTCATCTGTTATATCTGAAAA 676
QY      201 AsnIlaSerThrGluTySerGlyThrTySerCysThrValIysAsnArgValIleGlySer 220
Db      677 AATGCTCTTCTGAGTACTCTGGACATACACCTGTACGTACAGAAACAGAGTGGCTCT 736
QY      221 AspGlnCysLeuLeuIleArgLeuAspValValProProSerAsnArgIleGlyThrIleAla 240
Db      737 GATCAGTGCCTGTTGCGTCTTAACGTTGCTCCCTCTTCAATTAACCTGGACATAATTGCA 796
QY      241 GlnAlaValIleGlyValLeuLeuIleAlaLeuValLeuIleGlyLeuIleIlePheCys 260
Db      797 GGAGCGCATTAATFAGAACTTTGCTGCTCTTAGCGCTCATTTGCTTATCATCTTTGCTGT 856
QY      261 Arg 261
Db      857 CGT 859

RESULT 14
US-09-989-734-504
; Sequence 504, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Auestin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

```

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/088217
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PRIOR APPLICATION NUMBER: 60/090535
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PRIOR APPLICATION NUMBER: 60/090542
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24

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2 PRIOR FILING DATE: 1998-06-25
3 PRIOR APPLICATION NUMBER: 60/090676
4 PRIOR FILING DATE: 1998-06-25
5 PRIOR APPLICATION NUMBER: 60/090630
6 PRIOR FILING DATE: 1998-06-25
7 PRIOR APPLICATION NUMBER: 60/090654
8 PRIOR FILING DATE: 1998-06-25
9 PRIOR APPLICATION NUMBER: 60/090655
10 PRIOR FILING DATE: 1998-06-25
11 PRIOR APPLICATION NUMBER: 60/090656
12 PRIOR FILING DATE: 1998-06-25
13 PRIOR APPLICATION NUMBER: 60/090682
14 PRIOR FILING DATE: 1998-06-26
15 PRIOR APPLICATION NUMBER: 60/090833
16 PRIOR FILING DATE: 1998-06-26
17 PRIOR APPLICATION NUMBER: 60/091360
18 PRIOR FILING DATE: 1998-07-01
19 PRIOR APPLICATION NUMBER: 60/091478
20 PRIOR FILING DATE: 1998-07-02
21 PRIOR APPLICATION NUMBER: 60/091544
22 PRIOR FILING DATE: 1998-07-01
23 PRIOR APPLICATION NUMBER: 60/091519
24 PRIOR FILING DATE: 1998-07-02
25 PRIOR APPLICATION NUMBER: 60/091626
26 PRIOR FILING DATE: 1998-07-02
27 PRIOR APPLICATION NUMBER: 60/091633
28 PRIOR FILING DATE: 1998-07-02
29 PRIOR APPLICATION NUMBER: 60/091978
30 PRIOR FILING DATE: 1998-07-07
31 PRIOR APPLICATION NUMBER: 60/091982
32 PRIOR FILING DATE: 1998-07-07
33 PRIOR APPLICATION NUMBER: 60/092182
34 PRIOR FILING DATE: 1998-07-09

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 11:49:47 ; Search time 1102 Seconds

(without alignments)
3835.773 Million cell updates/sec

Title: US-09-899-634C-2

Perfect score: 1359

Sequence: 1 MALLLFRVLICGVADLTRSL.....AVIGVLALVIGLIIIFCCR 261

Scoring table:

BLAST62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xih
-O=lcgnt 1/USPTO.spool/US09899634.rnat 09072003 111139 16356/app.query.fasta.1.455
-DB=EST -OQMT=fastap -SUFFIX=ret -MINMATCH=0.1 -TOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=D10sum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09899634.CCGN 1.1 1456 @rnat 09072003 111139 16356 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1238 | 91.1 | 917 | 9 | AL521066 |
| 2 | 1216 | 89.5 | 2731 | 11 | AK004908 |
| 3 | 1197 | 88.1 | 1022 | 13 | BM547121 |
| 4 | 1136.5 | 83.6 | 864 | 13 | BM84437 |
| 5 | 1129.5 | 83.1 | 922 | 13 | BM74365 |
| 6 | 1105 | 81.3 | 879 | 9 | AU131437 |
| 7 | 1084 | 79.8 | 956 | 13 | BM69353 |
| 8 | 1060 | 78.0 | 824 | 9 | AL534436 |
| 9 | 1049 | 77.2 | 775 | 13 | BM87131 |
| 10 | 1019 | 75.0 | 779 | 13 | BM80376 |
| 11 | 1015 | 74.7 | 885 | 9 | AL555497 |
| 12 | 1004 | 73.9 | 680 | 13 | BM537136 |
| 13 | 935 | 68.8 | 885 | 13 | BM83597 |
| 14 | 913.5 | 67.2 | 702 | 13 | BM77977 |
| 15 | 909.5 | 66.9 | 838 | 9 | AL514786 |
| 16 | 890 | 65.5 | 677 | 10 | BB865941 |
| 17 | 864.5 | 63.6 | 753 | 10 | BE545085 |
| 18 | 855.5 | 63.0 | 915 | 14 | BQ895050 |
| 19 | 855 | 62.9 | 727 | 12 | BM718557 |
| 20 | 843 | 62.0 | 644 | 10 | BB866153 |
| 21 | 824 | 60.6 | 831 | 9 | AL709335 |
| 22 | 818 | 60.2 | 928 | 12 | BF583890 |
| 23 | 789.5 | 58.1 | 1240 | 14 | BM804211 |
| 24 | 748 | 55.0 | 970 | 12 | BF164005 |
| 25 | 746 | 54.4 | 557 | 14 | BM750447 |
| 26 | 739.5 | 54.1 | 552 | 10 | AV605585 |
| 27 | 721 | 53.1 | 499 | 12 | BF441041 |
| 28 | 679 | 50.0 | 532 | 12 | BF015855 |
| 29 | 653 | 48.1 | 562 | 10 | AME59949 |
| 30 | 630 | 46.4 | 632 | 10 | BE543957 |
| 31 | 611 | 45.0 | 643 | 10 | BE303495 |
| 32 | 608.5 | 44.8 | 667 | 10 | BE292163 |
| 33 | 599 | 44.1 | 381 | 14 | W39780 |
| 34 | 584 | 43.0 | 921 | 14 | BQ955130 |
| 35 | 579.5 | 42.6 | 632 | 9 | AL655801 |
| 36 | 543.5 | 40.0 | 643 | 13 | BI082555 |
| 37 | 539 | 39.7 | 393 | 14 | N31467 |
| 38 | 520 | 38.3 | 356 | 12 | BF553315 |
| 39 | 517.5 | 38.1 | 439 | 14 | C16023 |
| 40 | 493.5 | 36.3 | 410 | 9 | AA474472 |
| 41 | 480.5 | 35.4 | 479 | 10 | BB860756 |
| 42 | 463.5 | 34.1 | 695 | 14 | BQ826547 |
| 43 | 454.5 | 33.4 | 417 | 9 | AA560303 |
| 44 | 447.5 | 32.9 | 657 | 9 | AL594052 |
| 45 | 443.5 | 32.6 | 537 | 13 | BG964235 |

ALIGNMENTS

RESULT 1
AL521066
LOCUS
DEFINITION
AL521066 LTI NFL004.NBC2 Homo sapiens cDNA clone CSDDB01VD23 5
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 917)
Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
Full-length cDNA libraries and normalization

Qy 241 G1yAlaValIleGlyValIleuAlaValIleuIleGlyLeuIleIlePheCysCys 260
 Db 807 GGGCCGCTCATAGGAGCGCTGCTGCTGCTCATCGGCGCATCTCTTCTGCTGT 866

RESULT 3
 LOCUS BM547121
 DEFINITION AGENCOURT 6499425 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5730154
 5', mRNA sequence.
 ACCESSION BM547121
 VERSION BM547121.1 GI:18780637
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1022)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM12728 row: j column: 11
 High quality sequence stop: 774.

FEATURES

source

1..1022 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5730154"
 /clone_1db="NIH MGC_124"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: EcoRV
 (destroyed); Site 2: NotI; RNA source male hippocampus,
 age 27. Library is oligo-dT primed and directionally
 cloned (EcoRV site is destroyed upon cloning). Average
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 012."

BASE COUNT 286 a 220 c 265 g 248 t 3 others

ORIGIN

Alignment Scores:

Pred. No.: 2.06e-125 Length: 1022
 Score: 1197.00 Matches: 231
 Percent Similarity: 92.78% Conservative: 13
 Best Local Similarity: 87.83% Mismatches: 17
 Query Match: 88.08% Indels: 2
 DB: 13 Gaps: 0

US-09-899-634c-2 (1-261) x BM547121 (1-1022)

Qy 1 MetAlaLeuLeuLeuCysPheValIleuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
 Db 149 ATGGCGCTCCCTGCTGCTGCTGCTGCTGCGAGAGTGGATTTCCGCAAGATTG 208

Qy 21 SerIleThrThrProGluGluMetIleGluLysAlaLysGlyGluThrAlaTyrLeuPro 40
 Db 209 AGTACTACTACTCTGAAGAGATGATTAAGAAAGCAAGGGAACCTGCTATCTGCA 268

Qy 41 CysArgPheThrLeuGlyProGluAspGlnLysProLeuAspIleGlyTyrLeuLeuSer 60
 Db 269 TGCAAAATTTCAGCTTACGTCGCCAAGGAGACCGCTGACATCGATGATATCA 328

Qy 61 ProAlaAspAsnGlnLysValaAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
 Db 329 CCAAGCTGATATATCAGAAAGGAGATCAAGTCATATTATTATCTCGAGCAAAATTAT 388

Qy 81 AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuSer 100
 Db 389 GATGACTACTATCATCAATCTGAAAGCCAGATCAATTTTACGATATGATGATCAATCT 448

Qy 101 G1yAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
 Db 449 GGTGATCATCATTAATGATGAAGATTTTCAACCTGATATTTGGCATATTCATGCTC 508

Qy 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLys 140
 Db 509 AAAGTGAAGAAAGCTCTGGTGTTCGCAATTAAGAAATTCATCTGTAGTTCTTGAAG 568

Qy 141 ProSerGlyThrArgCysTyrValaAspGlySerGlnGlnIleGlyAsnAspPheLys 160
 Db 569 CTTTCAGGTGCGAAGTTCATGTTGATGATCTGAAGAAATGGAAGTGCCTTAAGATA 628

Qy 161 LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
 Db 629 AAATGCAACCAAAAGAGTTCACTTCCATTACATATGATGCGCAAAATTTCTGTAC 688

Qy 181 SerGlnLysLeuProThrLeuTyrLeuAlaGluMetThrSerProValIleSerValLys 200
 Db 689 TCACAGAAATGCGCACTTCATGCTTACGGAATGATCATCTGTATATCTGTAAAA 748

Qy 201 AsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGlySer 220
 Db 749 AATGCCCTTCTGATGACTCTGGACATACAGCTGACATGCAAGAGGCGCTCT 808

Qy 221 AsnGlnCysLeuLeuArgLeuAspValVal-ProProSerAsnArgAlaGlyThrIleAl 240
 Db 809 GATCAGTGCCTGTTGCTGCTCAAAAGTTGCCCTCTCTCAAAATGCTGACTAATTC 868

Qy 240 acly-AlaValIleGlyValIleuAlaValIleuIleGlyLeuIleIlePheCysC 260
 Db 869 AGAGNCATATATGAGGACTTCTGCTGCTACGCTCATGTGNCATTATCATCTTTGCT 928

Qy 260 yAsArg 261
 Db 929 GGGCN 933

RESULT 4

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bi684437 864 bp mRNA linear EST 18-SEP-2001
 603308304F1 NCI_CGAP_Mame Mus musculus cDNA clone IMAGE:5344176 5',
 mRNA sequence.
 ACCESSION Bi684437
 VERSION Bi684437.1 GI:15647065
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 864)
 NIH-MGC http://mgi.nci.nih.gov/.
 Tissue Procurement: Jeffrey Green M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM11874 row: h column: 01
 High quality sequence stop: 855.
 Location/Qualifiers
 1..864


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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5344176"
/clone_lib="NCI CGAP Mam6"
/sex="Female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      223 a      225 c      222 g      194 t
ORIGIN

Alignment Scores:
Pred. No.:      1,2e-118      Length:      864
Score:          1136.50      Matches:      221
Percent Similarity: 90.04%      Conservative: 14
Best Local Similarity: 84.67%      Mismatches: 24
Query Match:      83.63%      Indels:      2
DB:              13          Gaps:          1

US-09-899-634C-2 (1-261) x B1684437 (1-864)

QY      1 MetAlaLeuLeuLeuCySpheValLeuLeuCyGlyValAlaAspLeuThrArgSerLeu 20
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Db      82 ATGGCGGGCTACTGTCCTTCCTGTCCTTGTGGCGGATTCGGGATTTCCACGAGGTTTG 141
QY      21 SerIleThrProGluGlnMetIleGlnValAlaGlyGlyGluThrAlaTYrLeuPro 40
      |||||
Db      142 AGCATCTACTACACCGCAACAGAGATCGAAAGCCAAAGGGGAACTGCGTATCTACCA 201
QY      41 CyArgpHeThrLeuGlyProGluAspGlnGlyProLeuAspIleGluThrPleuLeuSer 60
      |||||
Db      202 TGCAGATTACTCTCACTCCGAGAACACAGGACCACTGACATGATGATGATGATATCC 261
QY      61 ProAlaAspAsnGlnValAspGlnValIleIleLeuTYrSerGlyAspIleTYr 80
      |||||
Db      262 CCCTGATATACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 321
QY      81 AspAspTYrTYrGlnAspLeuGlyValArgValHisPheThrSerAsnAspLeuYSer 100
      |||||
Db      322 GATAACTACTATCCGATCGATCGAAAGGAGGATGATGATGATGATGATGATGATGATGAT 381
QY      101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyTYrTYrGlnGly 120
      |||||
Db      382 GGGGACGATCTTAAATGATGACCACTGATGATGATGATGATGATGATGATGATGATGATG 441
QY      121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
      |||||
Db      442 AAAGTGAAGAAAGCCCTGGGGTTGCAAAATGAATTCCTCGTACCGCTTCTGTATAG 501
QY      141 ProSerGlyThrArgCYrTYrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
      |||||
Db      502 CCTTCAGTACAAAGATGCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 561
QY      161 LysCysGluProLysGlyGlySerLeuProLeuLeuTYrGluTYrGlnLysLeuSerAsn 180
      |||||
Db      562 AAATGTAAACCAAGAGAGGCTCCCTTCCTCACTGATGATGATGATGATGATGATGATGAT 621
QY      181 SerGlnLysLeuProThrLeuThrPleuAlaGlnMetThrSerProValIleSerValLys 200
      |||||
Db      622 TCCCAAGCAATGCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
QY      201 AsnAlaSerThrGluTYrSerGlyTYrTYrSerCys--ThyVal---LysAsnArgValG 219
      |||||
Db      682 AAGCCAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741
QY      219 YSerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGlyThrT 239
      |||||
Db      742 CTGTGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 801

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QY      239 eAlaGlyAlaValIleGlyValLeuLeuAlaLeuValLeuIleGlyLeuIleIlePecy 239
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Db      802 CCGGGGCGCCCTCATATGAGGACGCTGCTGCTGTGCTATCATCGGGGACATCTTCTGTG 861
QY      259 s 259
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Db      862 T 862

RESULT 5
BI754365
LOCUS   BI754365
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 922)
NIH-MGC http://mgi.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Place: LLM11494 row: c column: 05
High quality sequence stop: 745.
Location/Qualifiers
1. 922
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5197372"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrigen). Research Genetics tracking code 019. Note:
this is a NIH MGC library."
BASE COUNT      274 a      199 c      207 g      242 t
ORIGIN

Alignment Scores:
Pred. No.:      8.38e-118      Length:      922
Score:          1129.50      Matches:      221
Percent Similarity: 90.49%      Conservative: 17
Best Local Similarity: 84.03%      Mismatches: 21
Query Match:      83.11%      Indels:      4
DB:              13          Gaps:          1

US-09-899-634C-2 (1-261) x B1754365 (1-922)

QY      2 AlALeuLeuLeuCySpheValLeuLeuCyGlyValAlaAspLeuThrArgSerLeu 21
      |||||
Db      2 GCGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 61
QY      22 IleThrThrProGluGlnMetIleGlnValAlaGlyGlyGluThrAlaTYrLeuProCys 41
      |||||
Db      62 ATCACTACTCTCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 121

```


Db 748 GATCAATGCTGCGCTTAAACGTGTCTCCCTTCAATTAAGCTGACTAATTGC 807

QY 240 aglyalavallieglyvalleuleuValleu 252
 Db 808 AAGGAGCCCATTTAGGACCTTTGGCTTGTCTTTA 844

RESULT 7
 BI649353
 LOCUS 603278089F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5318302 5', mRNA sequence.
 ACCESSION BI649353
 VERSION BI649353.1 GI:15563589
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 956)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.liml.gov
 Plate: LIML1807 row: a column: 23
 High quality sequence stop: 797.

FEATURES
 source
 1..956
 /organism="Mus musculus"
 /strain="129,C57BL/6J,FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5318302"
 /clone_lib="NCI CGAP Mam3"
 /tissue_type="tumor_gross tissue"
 /dev_stage="10 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

BASE COUNT 253 a 242 c 251 g 210 t

ORIGIN

Alignment Scores:
 pred. No.: 1.34e-112 Length: 956
 Score: 1084.00 Matches: 226
 Percent Similarity: 89.96% Conservative: 16
 Best Local Similarity: 84.01% Mismatches: 18
 Query Match: 79.76% Indels: 9
 DB: 13 Gaps: 0

US-09-899-634c-2 (1-261) x BI649353 (1-956)

QY 1 MetAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuValAlaLeuLeuThraXsSerLeu 20
 Db 97 ATGGCGCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 156
 QY 21 SerIleThrThrProGluGlnMetIleGluLysAlaLysGlyLysThrAlaTyrLeuPro 40
 Db 157 AGCATCACTACACCCGAAACAGAGATCGAAAGCCAAAGGGAAGTGGTATCAACA 216
 QY 41 CysArgPheThrLeuGlyProGluLysArgGlyProLeuAspIleGluTyrPleuLeuSer 60
 Db 217 TGGAAATTACTCTCACTCCCGAAGACCAAGGACCACTGACATGTAATGGCTGATATCC 276

QY 61 ProAlaAspAsnGlnLysValAlaAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
 Db 277 CCCTGTGATPACACAGATAGATGATCAAGTATCATTTTGTATCTCGAGCAAAATTTAT 336
 QY 81 AspAspTyrTyrGlnLeuLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
 Db 337 GATAACTACTATCTCCGATCTGAAAGACCGGTACATTTACGATACGATGCAAGTCT 396
 QY 101 GLYAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
 Db 397 GCGACGACATCTATAATGATGACCAACCTGCACCTCGGACATGACACTTACCCAGTGC 456
 QY 121 LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLeuLys 140
 Db 457 AAGTGAAGAAAGCCCTCGGCGTTGCAATTAAGAAATTCCTGTCACCGTTCTGTTAAG 516
 QY 141 ProSerGlyThrArgCysTyrValAlaAspGlySerGluIleGlyAsnAspPheLysLeu 160
 Db 517 CCTTCAGGTACAAGATGCTTCGATGATGATCGAAGAGATTGGAATGACTTCAAGCTTA 576
 QY 161 LysCysGluProLysGlnGlySerLeuProLeu-LeuTyrGluTyrGlnLysLeuSerAs 180
 Db 577 AATGTGAACCCAGAGAAAGCTCCCTTCACACTACACTTTGAATGGCAGAACTGTGCA 636
 QY 180 nSerGlnLysLeuProThrLeuTyrPheAlaGlnMetThrSerProValIleSerValLys 200
 Db 637 CTCGCCAGACAAATGCTCAACCCATGCTGCGCAGAAAGACGTACCACTATATCTGTGA 696
 QY 200 AsnAlaSerThrGlu-TyrSerGlyThrTyrSerCysThrValLysAsnArgValGlyS 220
 Db 697 GAACGCCAGTTCAGTAATTTCTGGGACATACAGCTGCACAGGTTCAAAACAGAGTGCG 756
 QY 220 eRAsp-GlnCysLeuLeuArgLeuAsp-ValValProProSerAsnArgAla-GlyThr- 238
 Db 757 CTGACCCAGTGTGCTGCGACAGCAAGTGTGCCACCTCAAAAGAGCCCGGAACGA 816
 QY 239 IleAlaGlyAlaValIleGlyVal--LeuLeuAlaLeuValLeuIle-GlyLeuIleIle 257
 Db 817 ATGGCGGCGCGCTGATAGGAAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 876
 QY 258 PheCysCys 260
 Db 877 TCTCTGCTGT 885

RESULT 8
 AL534436
 LOCUS AL534436 LIT_FLO13_FBRn1 Homo sapiens cDNA clone CS0DF004YB08 5 prime, mRNA sequence.
 ACCESSION AL534436
 VERSION AL534436.1 GI:12797929
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 824)
 Li,W.B., Gruber,C., Jessee,J. and Poyajes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT Contact: Genoscope - Centre National de Sequencage
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr.

FEATURES
 source
 1..824
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DF004YB08"
 /clone_lib="LIT_FLO13_FBRn1"
 /dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"

/lab host="DH10B"
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by Life
 Technologies. Contact : Feng Liang Life Technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 Maryland 20850, USA Fax : (1) 301 610 8371 Email :
 fliang@life.com
 http://fulllength.invitrogen.com"

BASE COUNT 257 a 163 c 149 g 236 t 19 others

ALIGNMENT SCORES:

Pred. No.: 5.66e-110 Length: 824
 Score: 1060.00 Matches: 200
 Percent Similarity: 93.39% Conservative: 12
 Best Local Similarity: 88.11% Mismatches: 15
 Query Match: 78.00% Indels: 0
 DB: Gaps: 0

US-09-899-634C-2 (1-261) x AL534436 (1-824)

QY 32 AAlaysglyguthrralatyrlleuProCysarphethrleuglyProgluaspdlgly 51
 DB 1 GCCAAGGGAACTGCTATCTGCGCATGCAATTTCAGCTTACCCGGAAGACAGGA 60
 QY 52 ProleuaspilleglutrleuLeuSerProAlaaspanglnlyValaspGlnVal 71
 DB 61 CCGCTGCGATCGAGTGGCTGATATCACACCTGATATCAGAAAGTGGATCAAGTATT 120
 QY 72 lileuutyrsrsglyaspilyselleTyrsaspyrtyrGlnaspilysglyAyrVal 91
 DB 121 ATTTATATCTGGAGACAAAATTATATATACATCAATCCAGATCTGAAGGCCGAGTA 180
 QY 92 HispethrSerAsnaspLeuLysSerGlyAspAlaSerIleasnValThrAsnLeuGln 111
 DB 181 CATTTCAGATATGATCTCAATCTGGTATGATGATCAATTAATGTAACAAATTTCAA 240
 QY 112 LeuSeraspilleglutythrGlnCysAllyVallyValaspGlyValaspGly 131
 DB 241 CTGTCAGATATGGACATATCAGTGCAGAAAGTGAAGAAAGTCTGCTGGTTCAGATTAAG 300
 QY 132 LysIleuglnleuThrValleuLeuLysProSerGlyThrArgCysTyrrValaspGlySer 151
 DB 301 AAGATCATCTGTGATGTTCTGTATAGCTTCAGGTGCGAATGTTAGTATGATGATCT 360
 QY 152 GluGlnIleGlyAsnaspPheLysLeuLysCysGluProLysGluGlySerLeuProleu 171
 DB 361 GAAGAAATTTGAGAGACTTAAAGTAAATGTAAGTGAACCAAGAAAGTTCCTCCATTA 420
 QY 172 LeuTyrglutrglnlyLeuSerAsnSerGlnLysLeuProThrLeuTrrleuLaglu 191
 DB 421 CAGATATGAGTGGCAAAATTTGCTGACTCACAGAAAGCCCACTTCAGTTCAGAGAA 480
 QY 192 MetThrSerProValIleSerVallyAsnAlaSerThrGluTyrrSerGlyThrTyrrSer 211
 DB 481 ATGACTTCATCTGTATATCTGTAAATAAATGCTCTTGTAGTACTTGGAGCATACAGC 540
 QY 212 CysThrVallyAsnAspValGlySeraspGlnCysLeuLeuArgLeuAspValValPro 231
 DB 541 TGTACAGTCAGAAACAGAGTGGCTCTCATCAGTCCCTGCTGCGTAAAGCTTCCT 600
 QY 232 ProSerAsnArgAlaglyThrIleAlaglyAlaValIleGlyValleuLeuAlaVal 251
 DB 601 CCTCAATAAAGCTGAGCTAATTCAGAGCCATTATAGGAACCTTCTTCCTACGCG 660
 QY 252 LeuIleGlyLeuIleIlePhe 258
 DB 661 CTCAATTCGCTTATCATCTTT 681

RESULT 9

B1687131
 LOCUS 775 bp mRNA linear EST 18-SEP-2001
 DEFINITION 603314974F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354827 5',
 mRNA sequence.
 ACCESSION B1687131 GI:15649759
 VERSION B1687131.1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 775)
 AUTHORS NIH-MGC
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM11902 row: c column: 20
 High quality sequence stop: 775.
 Location/Qualifiers

FEATURES

source

1..775
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5354827"
 /clone_lib="NCI CGAP Mam6"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 213 a 193 c 192 g 177 t

ALIGNMENT SCORES:

Pred. No.: 9.13e-109 Length: 775
 Score: 1049.00 Matches: 205
 Percent Similarity: 92.83% Conservative: 15
 Best Local Similarity: 86.50% Mismatches: 15
 Query Match: 77.19% Indels: 3
 DB: Gaps: 0

US-09-899-634C-2 (1-261) x B1687131 (1-775)

QY 1 MetAlaleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
 DB 70 ATGGCGGCGCTATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129
 QY 21 SerIleThrThrProGluGlnMetIleGlnlyValaspGlyValaspGlyValaspGly 40
 DB 130 AGCATCTACTACCCGGAACAGAGATCGAAGAAAGCCAAAGGGGAAACCTGGGTATCAACA 189
 QY 41 CysArpethrleuGlyProgluaspGlnGlyProleuaspilleglutrleuLeuSer 60
 DB 190 TGCAGTTTACTCTCACTCCGGAAGACCA-GAACCTGAGCATTTGAATGCTGATATCC 248
 QY 61 ProAlaaspanglnlyValaspGlnValIleIleLeuTyrrSerGlyaspIleTyrr 80
 DB 249 CCGCTGATACACGAGATGAGTCAAGTATATTTGATTTCTGAGACAAATTTAT 308
 QY 81 AspaspTyrrtyrGlnaspLeuLysGlyAyrValHispethrSerAsnaspLeuLysSer 100
 DB 309 GATAACTTATATCCGATCGAATGAAAGACGGGTACATTTTACAGATACGATGTCAGATCT 368

QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTygIncys 120
Db 369 GCGGACGACCTATTAATGATGACCACTGACGAGTTCGACATTGGCACTTCCAGTGC 428
QY 121 LysValLysValAlaProGlyValGlyAsnLysIleGlnLeuThrValLeuLys 140
Db 429 AAGTGAAGAAACCCCTGGGGTTCGAAATGAATAATTCCTGCTGACCGTCTTGTTAAG 488
QY 141 ProSerGlyThrArgCysTyValAlaAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
Db 489 CTTTCAGGTCAAGATGCTTCGTGATGATCGAAGAGATGGAATGACTTCAAGCTA 548
QY 161 LysCysGluProLysGluGlySerLeuProLeuLeuLysIleGlnTygIncysLeuSerAsn 180
Db 549 AATATGAAACCAAGAGAGGCTCCCTTCCACTACAGTTGAATGGCAGAAAGTGTGGAC 608
QY 181 SerGlnLysLeuProThrLeuThrLeuAla-GluMetThrSerProValIleSerVally 200
Db 609 TCCACAGACATGCTTACGCGCATGCTGGCAGCAAAATGACCTCACAGTTATATCTGTGA 668
QY 200 AsnAlaSer-ThrGluTySerGlyThrTySerCysThrValLysAsnArgValGlyS 220
Db 669 GAACGCCAGTTCTGAGTATTCGGGACATACAGCTGCACGTTCAAAACAGAGTGGCT 728
QY 220 exAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArg 235
Db 729 CTGACCAAGTGTATGCTGCGACCTAGACGTTCTCCACCCCTCAACCGA 775
RESULT 10 779 bp mRNA linear EST 20-JUN-2001
LOCUS BI080376 60287628B1 NC1_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008543 5'
DEFINITION mRNA sequence.
ACCESSION BI080376
VERSION BI080376.1 GI:14498706
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 779)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM1053 row: 9 column: 08
High quality sequence stop: 767.
Location/Qualifiers
1..779
/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone_1ib="IMAGE:5008543"
/clone_1ib="NCI CGAP Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT
ORIGIN

212 a 196 c 195 g 176 t

Alignment Scores:

Pred. No.: 2,39e-105 Length: 779
Score: 1019.00 Matches: 202
Percent Similarity: 92.02% Conservative: 17
Best Local Similarity: 84.87% Mismatches: 14
Query Match: 74.98% Indels: 5
DB: 13 Gaps: 0

US-09-899-634c-2 (1-261) x BI080376 (1-779)

QY 1 MetAlaLeuLeuLeuCysPheValLeuLeuCysGlyValAlaAspLeuThrArgSerLeu 20
Db 74 ATGGCGCGCCTACTGCTGCTTCGCTTCGTGTGGGGATCGGATTTCCACAGTGGTTTC 133
QY 21 SerIleThrThrProGluGlnMetIleGluValAlaLysGlyGluThrAlaTyLeuPro 40
Db 134 AGCATCACTACACCCGACAGAGATCGAAGAAAGGAGAACTGGTATCTTACCA 193
QY 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluThrLeuLeuSer 60
Db 194 TGCAGTTTACTCTCAGTCCCGAAGACAGGAGCCACTGGACATTGAATGGCTGATATCC 253
QY 61 ProAlaAspAsnGlnLysValAlaAspGlnValIleLeuTySerGlyAspLysIleTy 80
Db 254 CGCTCGATTAACCAAGATGATGATCAAGATCATTTTGTATCTGGAGACAAATTTAT 313
QY 81 AspAspTyThrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
Db 314 GATTACTACTATCCGATCTGAAAGAGCGGATATTTCAGATACAGATGTCAGTCT 373
QY 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTygIncys 120
Db 374 GCGGACGACCTATTAATGATGACCACTGACAGCTGTCCGACATTGGCACTTACAGTGC 433
QY 121 LysValLysValAlaProGlyValGlyAsnLysIleGln-LeuThrValLeuLeuLys 140
Db 434 AAGTGAAGAAACCCCTGGGGTTCGAAATGAAGAAATTCCTGCTGACCGTCTGTGA 493
QY 140 ProSerGlyThrArgCysTyValAlaAspGlySerGluGluIleGly-AsnAspPheLysLeu 160
Db 494 GCTTCAGGTACAAAGTGTCTGTGATGATCGAAGAGATTGCAATGACTTCAAGC 553
QY 160 eulLysCysGluProLysGluGlySerLeuProLeuLeuLysIleGlnTygIncysLeuSer 180
Db 554 TAAATGTAACCAAGAGAGGCTCCCTTCCACTACAGTTGAATGGCAGAAACTGTGG 613
QY 180 snSerGlnLysLeuProThrLeuThrLeuAla-GluMetThrSerProValIleSerVal 199
Db 614 ACTCCAGACAAATGCTTACGCGCATGCTGGCAGCAAAATGACCTCACAGTTATATCTGTG 673
QY 200 LysAsnAlaSer-ThrGluTySerGlyThrTySerCysThrValLysAsnArgVal-GI 219
Db 674 AAGAACGCCAGTTCGAGTATTCGGGACATACAGTGCAGGTTCAAAACGAGTGGG 733
QY 219 ySerAsp-GlnCysLeuLeuArgLeuAspValValProProSer 233
Db 734 CTCTGAACCAAGTGTATGCTGCCACTAGACGTTCTCCACCTTCC 777
RESULT 11
LOCUS AL555497 885 bp mRNA linear EST 16-FEB-2001
DEFINITION AL555497 LRI_NFL006_PL2 Homo sapiens cDNA clone CSDDK008Y07 5
prime, mRNA sequence.
ACCESSION AL555497
VERSION AL555497.1 GI:12897284
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 885)
REFERENCE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization

JOURNAL
COMMENT

Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source

1. .885
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS00K008P07"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life technologies, a division of invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 272 a 182 c 190 g 237 t 4 others

Alignment Scores:

Pred. No.: 8,45e-105 Length: 885
Score: 1015.00 Matches: 191
Percent Similarity: 93.95% Conservative: 11
Best Local Similarity: 88.84% Mismatches: 13
Query Match: 74.69% Indels: 0
DB: 9 Gaps: 0

US-09-899-634C-2 (1-261) x AL555497 (1-885)

47 ProGUaspGnglyProLeuaspIegluTrpleuSerProaIaspasngluys 66
Db 6 CCCGAAACGACGAGCCGTCGATCATCGATGATATCACCAGCTGATATCAGAAG 65
Qy 67 ValaspInvalIelleleuTySerGlyaspIysIetyraapayTyTyGlnasp 86
Db 66 GTGATCAAGATATTTATTTATTTATTTCTGGAACAAATTAATGATGATATTCAGAT 125
Qy 87 LeuysgIyArvAHisPheThSerAsnaspLeuysSerGlyaspAsnSerIAsn 106
Db 126 CTGAAGGCCGAGACATTTTACAGATATATCTCAATCTGATGATCATCAATTAAT 185
Qy 107 ValThrasnleuGlnleuSeraspIeglyThTyGnglyValIyValIyAsn 126
Db 186 GTAACGAATTTACAACTGTGATATTTGGCACATATCATCAAGTCAAAAGAAAGCTCCT 245
Qy 127 G1yValAlGlyasnlysvIleGlnleuThValIleuLeuysProSerGlyThArgCys 146
Db 246 GGTGTTCAAATTAAGAAATTCATCTGTAGTTCTTTGTTAAAGCCTTCAAGTGCAGATGT 305
Qy 147 TyValaspGlySerGluGluIleGlyAsnaspPheIyLeuIyCysGluProIyGlu 166
Db 306 TACCTTATGATCTGAAGAAATTTGAAGTCACTTTAAGATTAATGTGAACCAAAAGAA 365
Qy 167 GlySerleuProleuLeuTyGluTrpGlnIyLeuSerAsnSerGlnIyLeuProThr 186
Db 366 GGTTCACCTTCATATACAGTATGAGTGGCAAMATTGCTGACTCAGCAAGAAATGCCACT 425
Qy 187 LeuTrpleuAlagIuMetThSerProValIleSerValIyAsnAlaserThGluTy 206
Db 426 TCATGGTTAGCAGAAATGACTTCACTCTATATCTGTMAAAVATGCTCTTCAGATAC 485
Qy 207 SerGlyThTySerCysThValIyAsnargValGlySeraspGlnCysLeuLeuArg 226
Db 486 TCTGGACATACAGCTGATCAGTCAAGAACAGAGGGCTCTGATCAGTGTGGTGT 545
Qy 227 LeuaspValIyProProSerAsnargAlagIyThIlealagIyAlaValIleGlyVal 246

Db 546 CTAACGTTGTCCCTCTTCAATAAAGCGACTAATTCGCGAGCCATTATAGAACT 605
Qy 247 LeuLeuAlaleuValleuIleGlyLeuIleIlePheCysCysArg 261
Db 606 TTCTTGCTCTACGCTCATGTGCTTATCATCTTTGCTGTCT 650

RESULT 12
BM537136 680 bp mRNA linear EST 20-FEB-2002
LOCUS ha78e07.g1 Canis cDNAs from testes cells Canis familiaris cDNA
DEFINITION clone ha78e07 5', mRNA sequence.
BM537136
VERSION BM537136.1 GI:18817097
KEYWORDS EST.
SOURCE dog.
ORGANISM Canis familiaris

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 680)
O'Shaughnessy, A.L., McCombie, W.R., Baker, J.P., Balija, V., Cummins
Kirchoff, K.A., Miller, B., Muller, S., Nascimento, L.U., Palmer, L.,
Santos, L., Shah, R.S., Spiegel, L.A., Zuber, T., Preston, R. and
Hannon, G.J.

Expressed sequence tags from Canis familiaris (dog) (2002)
Unpublished (2002)
Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ha78 row: e column: 07
Seq primer: -21M13univRev
High quality sequence stop: 680.

FEATURES
source

1. .680
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone="ha78e07"
/clone_lib="Canis cDNAs from testes cells"
/tissue_type="testes"
/note="Vector: Lambda Zap II; The library was produced by Greg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using strategene zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

BASE COUNT 206 a 155 c 151 g 168 t

ORIGIN

Alignment Scores:
Pred. No.: 9.72e-104 Length: 680
Score: 1004.00 Matches: 191
Percent Similarity: 95.15% Conservative: 5
Best Local Similarity: 92.72% Mismatches: 10
Query Match: 73.88% Indels: 0
DB: 13 Gaps: 0

US-09-899-634C-2 (1-261) x BM537136 (1-680)

Qy 1 MetAlaleuLeuLeuCyPheValleuLeuCyGlyValAlaspLeuThArgSerLeu 20
Db 61 ATGCGCTCTCTGCTGCGCTTCTGCTCTCTGCGAGTCCGGAATTCACAGAAAGTTG 120
Qy 21 SerIleThThProGluGlnMetIleGluValAlaysgIyGluThralaTyLeuPro 40
Db 121 AGTATCACTACTCTCTTAACAGATGATGAAAGCCAAAGGGAAGTCTTATTTGCCA 180
Qy 41 CysArgPheThLeuGlyProGUaspGnglyProLeuaspIleGluTrpleuLeuSer 60
Db 181 TGCAAATTTACCTTATGTCAGAAAGACAGAGGACCCCTGAGATCATCAGTGTGCTGTCA 240

| | | | |
|----|-----|---|-----|
| OY | 61 | ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr | 80 |
| Db | 241 | CCAGTGAATATCAGAAAGGTGACCAAGTGAATTTATTTATTTCTGGACCAAAATTTAT | 300 |
| OY | 81 | AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer | 100 |
| Db | 301 | GACGCTCTCTATCAAGATCTGAAAGAGCAGATGACATTTTACAAGCAATGATCTCAATCT | 360 |
| OY | 101 | GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys | 120 |
| Db | 361 | GGTATGATCATTAATATGTAACCAATTTACGGTGTGCAGATATGGCACATACAGATGC | 420 |
| OY | 121 | LysValLysLysAlaProGlyValGlyAsnLysLysIleGlnLeuThrValLeuLysLys | 140 |
| Db | 421 | AAAGTGAAGAAAAAGCTCCTGGTGTGGAAATAAGAAAGATTCACTGACAGTTCTTGTTAAG | 480 |
| OY | 141 | ProSerGlyThrThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu | 160 |
| Db | 481 | CCTTCAGGTATTAAGATGTTACCGTTATGATGATCAGAAAGAAATGCACCTTTAAACTTA | 540 |
| OY | 161 | LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluThrGlnLysLeuSerAsn | 180 |
| Db | 541 | AAATGTGAACCAAAAGAAAGTTCACTTCATTCATCAATATGAATGGCAAAAATTTGCCAAT | 600 |
| OY | 181 | SerGlnLysLeuProThrLeuThrLeuAlaGluMetThrSerProValIleSerValLys | 200 |
| Db | 601 | TCACAGAAACGCCCCCTCGGTGTCACACAGATATGACTTCACCTGTATATCATATAAAA | 660 |
| OY | 201 | AsnAlaSerThrGluTyr | 206 |
| Db | 661 | AATGGCTCTACTGAGATAC | 678 |

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RESULT 13
BI823597
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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BI823597 885 bp mRNA linear EST 04-OCT-2001
 603040961F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181807 5',
 mRNA sequence.
 BI823597
 BI823597.1 GI:15935147
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 885)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: LLM11453 row: j column: 16
 High quality sequence stop: 705.
 location/Qualifiers
 1..885

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5181807"
/clone_lib="NIN MGC_115"
/lab host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pcwv-spcr6; Site_1: NCBI; Site_2: ECoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
0.33x10^6 pfmed and directionally cloned (ECoRV site is
destroyed upon cloning). Average insert size 1.8 kb."

```

| BASE COUNT | ORIGIN |
|------------|-------------------|
| 263 a | 191 c 216 g 215 t |

insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."

| Alignment Scores: | |
|------------------------|----------|
| Pred. No.: | 1,08e-95 |
| Score: | 935.00 |
| Percent Similarity: | 84.564 |
| Best local Similarity: | 79.154 |
| Query Match: | 68.804 |
| DB: | 13 |

US-09-899-634C-2 (1-261) x B1823597 (1-885)

| | Length: | 885 |
|--|---------------------------|-----|
| | Matches: <td>205</td> | 205 |
| | Conservative: <td>14</td> | 14 |
| | Mismatches: <td>28</td> | 28 |
| | Indels: <td>14</td> | 14 |
| | Gaps: <td>4</td> | 4 |

| LOCUS | DEFINITION | EST 2001 |
|-------|--|----------|
| Oy | 1 Met1a1euleuleuLeuCySPheVal1euleuYsg1Val1a1aaspLeuThArgSer1eu | 20 |
| Db | 77 ATGGCGCTCCTCGCTGCTCTGCTCTCTCTGCGGAGTAGTGGATTTCGCCAAGTTTG | 136 |
| Oy | 21 Ser1eThrThrProGluGlnMet1eGlu1uys1a1a1ySG1guThrAla1TyR1euPro | 40 |
| Db | 137 AGTATCTACTACTCTCGAAGAGATGATTGAAGAAACCCAAAGGGGAAACCTGATTCTGCCA | 196 |
| Oy | 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAsp11eGluThrLeuLeuSer | 60 |
| Db | 197 TGCMAATTTCAGCTTAAGTCCCGAAGACCA -GGACCGCTGGACATCGAGTGGCTGATATCA | 255 |
| Oy | 61 Pro1a1aSPaeng1uys1a1aSPGlnVal11e1leuThySerG1yAsp1y1e1Ty | 80 |
| Db | 256 CCACCTGATATATCAGAAGGTGATCAAGATGATTATTATATTCCTGGAGACAAATTTAT | 315 |
| Oy | 81 AspAsp -TyR1TyR1GlnAspLeuLeuYsg1ArgVal1HisPheThrSerAsnAspLeuYse | 100 |
| Db | 316 GATACCTGACTATCCAGATCTGGAAGGCCGAGTACATTATTCAGATATGATCTTCAATTC | 375 |
| Oy | 100 rG1yAspAlaSer11eAsnVal1ThrAsnLeuGlnLeuSerAsp11eGlyThrTyR1GlnCy | 120 |
| Db | 376 TGGTGAATGCATCATTAATGTAATGTAAGAAATTATCAACTGTACATATTTGGCATATCAGTG | 435 |
| Oy | 120 b1ySVa11y1a1aP1oG1yVal1G1yAsn1y1e11eGln1euThrVal1euleu1y | 140 |
| Db | 436 CAAAGTAAAAAAGCTCTGCTGTTGCAATATMAAGAAATTCATCTGGAGTCTTGTTTAA | 495 |
| Oy | 140 sP1oSerG1yThrArgCys1TyR1a1aSPG1SerG1Glu11eG1yAsnAspPhe1y1e | 160 |
| Db | 496 GCCTTCAGGTCGAGATGTTTACCTGATGATCTGAAGAAATTGGAACTGACTTTAAGAT | 555 |
| Oy | 160 u1yCySG1uP1o1ySG1u1ySer1euP1oLeuLeuTyR1uThP1o1y1e1uSer1a | 180 |
| Db | 556 AAATGTGAACCAAAAGAGTTCACTTCCATTACAGTATAGTGGCAAAATAGTGTGCA | 615 |
| Oy | 180 nSerG1u1yLeuP1oThrLeuThP1e1u1a1aGlu -MetThSerP1roVal11eSerVal1 | 200 |
| Db | 616 CTCACAGAAATGCCACTTCATGTTAAGCAACATGACTTCAATCTGTCATATCTGTTA | 675 |
| Oy | 200 ySaSnAlaSerThGluTyR1SerG1yThrTyR1Ser -CysThrVal1y1s ---AsnArgVal | 218 |
| Db | 676 AAATATGC -TCTTTCAGAGTACTCTGGACATACACCTTGATCCGCTCGAAGAACAGAAAG | 734 |
| Oy | 219 G1y-----SerAspGlnCy---LeuLeuArgLeuAspValValProProSer | 233 |
| Db | 735 GGACCTCATGATCTCCAGATGACATGTGGGTATTAAGAGTTGGTCCCTCTT ---TCA | 788 |
| Oy | 234 Asn -ArgAlaG1yThr11eAlaG1yAlaVal11eG1yVal1euleu1a | 249 |
| Db | 789 AATCAAGCTGGACTAATTGACAGACACTTATTAAGAACTTGCTGGCA 837 | |

mRNA sequence.
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 VERSION BI077977.1 GI:14496307
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 702)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: rgsb@lemail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: LLNL1047 row: a column: 07
 High quality sequence, stop: 700.
 Location/Qualifiers
 1..702
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 /strain="FVB/N-3"
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 /clone="IMAGE:5006094"
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 /dev_stage="5 months"
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 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
 BASE COUNT 197 a 172 c 173 g 160 t
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 Alignment Scores:
 Pred. No.: 2.05e-93 Length: 702
 Score: 913.50 Matches: 180
 Percent Similarity: 91.47% Conservative: 13
 Best Local Similarity: 85.31% Mismatches: 16
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 21 SerIleThrThrProGluGlnMetIleGluValAlaIleGlyGluThrAlaTyrLeuPro 40
 131 AGCATCACTACACCGCAAGAGATCGAAAAGGCAAGGGAAGCTGCTACTACCA 190
 41 CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTyrLeuLeuSer 60
 191 TGCAAGTTTACTCTCAGTCCGAAAGACCA-GGACCACCTGGAATTGATGCTGATATCC 249
 61 ProAlaAspAsnGlnValAspGlnValIleIleLeuTyrSerGlyAspValIleTyr 80
 250 CCGTGTGATTAACCGATATGATGATCAATTTGATTTCTGGAGACAAATTTAT 309
 81 AspAspTyrTyrGlnAspLeuIleGlyValArgValHisPheThrSerAsnAspLeuLeuSer 100
 310 GATTAACACTACTCCGATCTGAAAGGACGGGTACTTTTACAGAAAGATGCTCAAGTCT 369
 101 GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
 370 GGCAGCGATCTATTAATGATGACCAACCTGACAGTGTGAGCAATTGACCTTACCAAGTGC 429

121 LysValIleValAlaProGlyValIleGlyAsnIleValIleGlnIleThrValLeuLeuLys 140
 430 AAAGTGAAGAAAGCCCTGGGGTTCGAAATTAAGAAATCTGCTGACCGTTCTGTAAAG 489
 141 ProSerGlyThrArgCysTyrValAlaAspGlySer---GluGluIleGlyAsn-AspPheIle 159
 490 CCTTCAGTGTCAAGATGCTTCGGAGATGATCGGCACACAGATTTGGAAACTGACTTCAA 549
 159 StLeuLysCysGluProGlySerLeuProLeuLeuTyrGluTyrGlnIleLeuLeuSer 179
 550 GCTAAATGTGAACCCAGAAAGGCTCTCTTCCACTACAGTTGAATGGCAAGAACTGTC 609
 179 AsnSerGlnIleLeuProThrLeuThrLeuAlaGluMetThrSerProValIleSerVal 199
 610 GCACTCCACAAACATGCTACGCGATGCTGCGCAAGAAATACCGTACCACTTATCTGT 669
 199 LysAsnAlaSerThrGluTyrSerGlyThr 209
 670 GAAGAACGCGAGTTCGATATCTGAGGACA 700
 RESULT 15
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 LOCUS AL514786 LTI_NFL006_PU2 Homo sapiens CDNA clone CLOBB015ZG03 5
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 ACCESSION AL514786
 VERSION AL514786
 KEYWORDS AL514786.1 GI:12778279
 SOURCE EST.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 838)
 REFERENCE 1 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1..838
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 /clone="CLOBB015ZG03"
 /clone_1lb="LTI_NFL006_PU2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 239 a 191 c 197 g 207 t 4 others
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 Alignment Scores:
 Pred. No.: 7.87e-93 Length: 838
 Score: 909.50 Matches: 180
 Percent Similarity: 81.51% Conservative: 14
 Best Local Similarity: 75.63% Mismatches: 30
 Query Match: 66.92% Indels: 15
 Gaps: 2
 DB: 9
 US-09-899-634c-2 (1-261) x AL514786 (1-838)
 1 MetAlaLeuLeuLeuCySPheValLeuLeuCySGlyValAlaAspLeuThrArgSerLeu 20


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Db      67  ATGGCGCTCCTGCTGCTGCTTCTGCTCTCTGCGGAGTAGTGATTTCCGACAGATTG 126
QY      21  SerIleThrThrProGluGlnMetIleGluLysAlaLysGluThrAlaTyrLeuPro 40
Db      127  AGTATCACTACTCTCTGAGAGATGATGAAAAAGCCAAAGGGAACTGCTTATCTGCCA 186
QY      41  CysArgPheThrLeuGlyProGluAspGlnGlyProLeuAspIleGluTyrLeuSer 60
Db      187  TGCAAATTACGCTTAGTCCCGAAGACGAGGACCCCTGACATCGAGTGGCTGATATCA 246
QY      61  ProAlaAspAsnGlnLysValAspGlnValIleIleLeuTyrSerGlyAspLysIleTyr 80
Db      247  CCAGCTGATATATCAGAAAGGTGATCAAGATATTTATATTTCTGAGACAAAATTAT 306
QY      81  AspAspTyrTyrGlnAspLeuLysGlyArgValHisPheThrSerAsnAspLeuLysSer 100
Db      307  GATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTTATGATCTCAAACT 366
QY      101  GlyAspAlaSerIleAsnValThrAsnLeuGlnLeuSerAspIleGlyThrTyrGlnCys 120
Db      367  GGTGATGATCAATTAATGATMACGAAATTTCACACTGTCAGATATTGGCACATATCAGTGC 426
QY      121  LysValLysLysAlaProGlyValGlyAsnLysIleGlnLeuThrValLeuLeuLys 140
Db      427  AAAGTGAATAAAGCTCTGAGTGTGCAATTAAGAAATTCATCTGTAGTTCCTGTTAG 486
QY      141  ProSerGlyThrArgCysTyrValAspGlySerGluGluIleGlyAsnAspPheLysLeu 160
Db      487  CCTTCAGGTGCGAGATGTTTCGTTGATGAGTCTGAAGAAATTTGGAAGTGACTTTAAGATA 546
QY      161  LysCysGluProLysGluGlySerLeuProLeuLeuTyrGluTyrGlnLysLeuSerAsn 180
Db      547  AATATGGAACCAAAAGAGGTTCACCTTCATTAAGATGAGTGGCAAAAATTTGCTGAC 606
QY      181  SerGlnLysLeuProThrLeuTyrPheAla---GluMetThrSerProValIleSerVal 199
Db      607  TCACAGAAATATGCCCACTTATGTTAGCAGGAAAGATGTG-CCACTCCAAAGAGCGGT 665
QY      200  LysAsnAlaSerThrGluTyrSerGlyThrTyrSerCysThrValLysAsnArgValGly 219
Db      666  ACGTCCACTGCCAGAGCTACATCGGCGATTATCATTCATCC-----707
QY      220  SerAspGlnCysLeuLeuArgLeuAspValValProProSerAsnArgAlaGly 237
Db      708  -----CTGGGGTCCATGTCTCTCCAAACATGGAAGGA 740
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Search completed: July 12, 2003, 12:59:45
Job time : 1110 secs

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